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1: geneseqp1980
2: geneseqp2000
3: geneseqp2000
4: geneseqp2001
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(c) 1993 - 2006 Biocceleration
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Adp75168			Ξ.	Adp75162	Aay72922	Aab80904	Aeb51285	Ξ.	Aaw49075	Aau81169	Abb73418	Aab16967	Aay96531	Abb73412	Aab16959		Abb73415	Aab16964	Abb73423	Aab17955
Fusion co	Human met	Human met	Recombina	Recombina	Recombina	Echistati	FC-EMP-EM	FC-EMP-EM	Human IgG	FC-TMP-TM	FC-TMP-TM	Amino aci	Fc-EPO mi	Fc-EMP pr	Fc-VEGF a	Fc-VEGF a				

ALIGNMENTS

AAY96529;

AAY96529 standard; protein; 228

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RESULT 1
AAY96529
ID AAY96529
XX AAY9
AC AAY9
XX Inmu
KW Inmu Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anaemic; dermatological; immunosuppressive; anti-inflammatory. Liu C, Homo WPI; 23-OCT-1998; 22-OCT-1999; 04-MAY-2000 WO200024770-A2 Human IgG1 Fc chain. 04-SEP-2000 (AMGE-) AMGEN 2000-365108/31. Feige U, (first 98US-0105348P 99WO-US024834. entry) ŗ,

Thrombopoietic peptides which activate mpl receptors and increase production of platelets or platelet precursors, useful for treatmediseases which involve thombocytopenia. the of.

N-PSDB;

AAA29220.

Disclosure; Page 76-77; 91pp; English.

A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1) nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising $x_2 - x_1$ 0, $x_2 - x_1$ 1, $x_2 - x_1$ 2, $x_2 - x_1$ 1, $x_3 - x_1$ 2, $x_3 - x_1$ 2, $x_3 - x_1$ 3, $x_3 - x_1$ 4, $x_3 - x_1$ 0, $x_3 - x_1$ 1, $x_3 - x_1$ 3, and $x_3 - x_1$ 3, $x_3 - x_1$ 4, $x_3 - x_1$ 5, $x_3 - x_1$ 6, $x_3 - x_1$ 7, $x_3 - x_1$ 7, $x_3 - x_1$ 8, $x_3 - x_1$ 8, $x_3 - x_1$ 8, $x_3 - x_1$ 9, $x_3 - x_1$ 8, $x_3 - x_1$ 9, $x_3 - x_1$ 9, $x_3 - x_1$ 1, $x_3 - x_1$ 2, $x_3 - x_1$ 3, $x_3 - x_1$ 1, $x_3 -$

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TTPO; CTLA4; mimetic; IL-1; TWF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
                                                                                                         Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
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22-OCT-1999;
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                                                   Claim 7; Page 176-177; 608pp; English
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)B; AAA69443.
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invention
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of matter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC (XI)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2-(L1)c-P1-(C2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, C2 (12)d-P2-(L3)e-P3, and L4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, C2 c, d, e, and f = are each independently 0 or 1, provided that at least 1 (C2 of a and b is 1. The composition can have cytostatic, antiasthmatic, C3 cells from the present invention can be used for producing pharmacoutical compositions are useful for treating cancer, asthma, C3 compositions. The compositions are useful for treating cancer, asthma, C4 chrombosis, or autoimmune diseases. The use of an Fc domain (rather than C4 a Fab domain) can provide a longer half-life or incorporate functions can be used for producing pharmacoutions are receptor binding, protein A binding, complement fixation, and composition at transfer. AaA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
              N-PSDB;
                             WPI; 2001-335908/35
                                                                                                                                                                                                                                                                                                  therapy; cancer; ost
transplant rejection
                                                                                                                                                                                                                                                                                                                 Human; IgG1; immunoglobulin; Fc region; Fc fusion protein; misfolding;
therapy; cancer; osteoarthritis; AIDS; obesity; inflammation;
                                                                                                                                                                                                                                                                                                                                                                 Human
                                                                                                                                                                                                                                                                                                                                                                                                                               AAB98953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB98953 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 228
                                                              Treuheit MJ,
                                                                                                                           09-NOV-2000; 2000US-00709704
                                                                                                                                        12-NOV-1999;
                                                                                                                                                                       10-NOV-2000; 2000WO-US030798
                                                                                                                                                                                                        17-MAY-2001.
                                                                                                                                                                                                                                      WC200134638-A1.
                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-2001
                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
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                                                                                             AMGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
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                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                              O'conner
                                                                                             INC.
                                                                                                                                                                                                                                                                                                                                                                 region
                                                                                                                                           99US-0165188P
                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                            SR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             228
                                                            Kosky AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1238; DB 3;
Pred. No. 4.6e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
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RESULT 4
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Best Local Sim:
Matches 228;
                                                                                                                                                                                                                                                                                                 Glucagon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a process for preparing a pharmacologically active compound, involving preparing a compound comprising an immunoglobulin Fc domain fused to a protein of interest, treating the compound with a copper(II) halide and isolating the treated molecule. This can be used to correct misfolding of Fc domain containing proteins, for use in therapeutic agents which may be used in the treatment of cancer, inflammation, transplant rejection, AIDS, osteoarthritis and obesity. The present sequence is the IgG1 Fc domain
  Claim 8;
                          diabetes
                                                                                                  Marshall
                                                                                                                                                03-MAY-2000;
02-MAY-2001;
                                                                                                                                                                                    03-MAY-2001; 2001WO-US014321.
                                                                                                                                                                                                             08-NOV-2001
                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                         ABB04279;
                                                                                                                                                                                                                                                                                                                                                                                               ABB04279 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 228 AA;
                                   Compositions comprising
                                                                                                                                                                                                                                                                                     non-insulin
                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Correcting disulfide bond misfolds in Fc-containing proteins, particularly therapeutic Fc-containing fusion proteins or antibodies,
                                                                                                                          (AMGE-)
                                                              2002-017738/02.
DB; ABA03672.
                                                                                                                                                                                                                                                             sapiens
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                                                                                                                          AMGEN
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                                                                                                 ws,
                                                                                                                                                                                                                                                                                 antagonist; antidiabetic; anti-hormonal; Fc domain;
lin dependent diabetes mellitus; human; immunoglobulin G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MDKTHTCPPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
Fig 2; 54pp; English
                          mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
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                                                                                                                                                 2000US-0201436P
2001US-00847249
                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                         INC.
                                                                                                 Stark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        copper halide.
                                                                                                                                                                                                                                                                                                                                                                                               protein;
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                                   glucagon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1238;
Pred. No. 4.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                ₿
                                     antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          = 1238; DB 4;
. No. 4.6e-90;
smatches 0;
                                     domains,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                      useful
                                      for
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ARESULT 5
AAUB1074
ID AAUB
XX AAUB
AC AAUB
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AC Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human
of the
                                                                                                                                                                                                                                                                                                                                                                              21-APR-2000; 2000US-0198919P.
03-MAY-2000; 2000US-0201394P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunosuppressive; ost
echistatin; integrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to compositions comprising a glucagon antagonist domain and a vehicle, such as a polymer (e.g. PEG or dextran) or, preferably, an Fc domain. The vehicle is covalently attached to the glucagon antagonist domain. The compositions are administered to treat non-insulin dependent diabetes mellitus. The present sequence is the human IgG Fc domain, which may be used as the vehicle in the compositions
                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; IgG Fc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human IgG1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200181377-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU81074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU81074 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 228 AA;
                                                                                                                                                                                                                                                                                                                                  (AMGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      angiogenesis; tumour;
                                                                                                                                                                                                                              2002-062025/08.
                                                                                                                                                                                                                                                                     Ċ,
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                                                                                                                                                                                                         ABK24097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
                                                                                                                                                                                                                                                                                Kohno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ive; osteopathic; antagonist; laminin; saw-scaled viper;
tegrin; selectin; vinculin; platelet aggregation;
tumour; inflammation; autoimmune disease;
hritis; osteoporosis.
                                                                                                                                                                                                                                                                           'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                Lacey
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Pred. No. 4.6e-90;
; Mismatches 0;
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Composition comprising integrin or adhesion vehicle, useful for treating or preventing planger half-life than free peptide.

platelet

antagonistic peptide platelet aggregation,

and has

ğ

The invention relates to a composition comprising

an integrin/adhesion

Claim 9;

Fig 3; 68pp;

English.

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RESULT 6
AAB14310
ID AAB1
XX AAB1
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XX Homo
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Best Local :
                                                                                                                                         03-MAY-2000; 2000US-0201511P
02-MAY-2001; 2001US-00847712
                                                                                                                                                                                                                                                                                                                                                                                               Human; calcitonin; CT; CT receptor; immunoglobulin G; IgG; osteopathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunoglobulin G (IgG1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
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ilarity 100.0%;
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Pred. No. 4.6e-90;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor; TNF-alpha inhibitor; interleukin 1 antagonist; TI-1 antagonist; TMP; TPO mimetic peptide; EPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to therapeutic agents that modulate the activity calcitonin (CT) receptor. Modulators of CT receptor comprise a CT receptor modulating domain and a vehicle such as a polymer or an FC domain, where the vehicle is covalently attached to the CT receptor modulating domain. The compositions comprising CT receptor modulating domain. The present sequence is human immunoglobulin G (IgG1) Fc protein used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Compositions comprising Calcitonin receptor modulator domains, useful treating osteoporosis.
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                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                          03-MAY-2000; 2000US-00563286
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                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombocytopaenia; metastatic
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Pred. No. 4.6e-90;
Mismatches 0;
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(AMGE-) AMGEN INC

(南)以传统者等是教徒一切成為

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RESULT 8
AAG66012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc neuroprotective activities. (1) can be used as a therapeutic or comprobective activities. (2) can be used as a therapeutic or cc prophylactic agent as well as for screening purposes. (1) is useful for cd diagnosing diseases characterised by dysfunction of their associated protein of interest, for identifying normal or abnormal proteins of compounds of interest in a biological sample. Additionally, (1) is useful cor treating inflammatory and autoimmune diseases, tumour growth, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders, infertility, and neurological degenerative diseases. (1), comprising EPO-compounds are useful for treating disorders compounds are useful for treating conditions that involve an existing megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic tumour which result in thrombocytopaenia, aplastic anaemia, metastatic tumour which result in thrombocytopaenia, aplastic anaemia, metastatic comprises syndrome. AbB73403 to AbB73426 and AbB135695 to AbB135777 represent amino acid and nucleic acid sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 228
                                                                    Apo-AI; amphipathic; anti-HIV; virucide;
                                                                                                                                                          27-FEB-2002
                                                                                                                                                                                                                              AAG66012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a vehicle-peptide molecule (I) or its multimers. (I) can have antiinflammatory, antitumour, immunosuppressive, cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological and antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                     181
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                                                                                                                     immunoglobulin
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                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                               SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                     SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSBGK 228
                                                                                                                                                                                                                                                                                                                                                                                                           KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
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                                                                                                                                                                                                                                                                                                                                                                                       KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
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                                                                                                                                                      (first
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                                                                                                                                                                                                                          protein;
                                                                    immunoglobulin;
                                                                                                                                                      entry)
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                                                                                  pharmaceutical; peptide mimic;
                                                                                                                   (Ig)
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Pred. No. 4.6e-90;
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                                                                                                                     region sequence.
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Best Local S
Matches 228
                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                      peptide mimic has greater half-life compared to conventional Apo-AI amphipathic helix peptide. The compositions are useful for treating hypercholesterolemia and viral infection such as HIV, HSV. The present
                                                                                                                                                                                                                                                                                                                                                                                               The invention provides a composition comprising a therapeutic agent has activity similar to Apo-Al amphipathic helix peptide, but with pharmaceutical characteristics attached to a vehicle through the peptide's N-terminus or C-terminus having a specified formula. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant or modified therapeutic agents having Apo-AI amphipathic helix peptide activity useful in treatment of hypercholesterolemia are viral infections such as herpes simplex virus, human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-2001
                                                                                                                                                                                                                                                                                                                                          sequence represents the human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-)
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DB; AAI67658.
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                                                                                                                                                                                                                                                     Similarity
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                                                       KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
                                                                                                                                    DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
                                                                                                                                                                                              MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                          SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                   DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                                                             MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                                                                                                                                                                                                                                                                228 AA;
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                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49pp;
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                                                                                                                                                                                                                                   Score 1238; DB 5;
Pred. No. 4.6e-90;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                       (Ig) G1 Fc region which acts
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                Length
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and

better

AAU73018 standard; protein; 228 AA.

120

60 60

(first entry)

Human immunoglobulin G (IgG) Fc region.

RRSULT 9
AAU73018
ID AAU7
XX AAU7
XX AAU7
XX BAU7
XX BAU7
XX BAU7
XX BAU7
XX Huma
XX Huma
XX PTHr
KW Calc
KW Calc
KW Dreas
XW Gauc
XW Frequ
KW Gauc
XW Frequ
KW Gauc
XW Frequ
KW Indmu Paget's disease; osteomyelitis; osteonecrosis; bone cell death; Gaucher's disease; sickle cell anaemia; systemic lupus erythema rheumatoid arthritis; periodontal disease; alopecia; fracture r Human; parathyroid hormone; PTH; parathyroid hormone-related protein; PTHr; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody; calcitonin, bisphosphonate; oestrogen; oestrogen receptor; tibolone; calcitonin; bisphosphonate; oestrogen; tumour metastasis; bone; osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone; breast cancer; prostate cancer; cachexia; anorexia; lupus erythematosus;
cia; fracture repair; osteoporosis;

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RESULT 10
ABJ38267
ID ABJ38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a composition (I) comprising modulators of parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHP) (C) which comprise a PTH/PTHP modulating domain and a vehicle. (I) (C) comprising PTH agonist optionally with a bone resorption inhibitor, such (C) as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates, (C) cestrogens, oestrogen receptor modulators and tibolone is useful for treating osteopenia. (I) is useful for therapeutic and prophylactic (C) purposes. Antagonists of PTH receptor are useful in treating primary and (C) secondary hyperthyroidism, hypercalcaemia, tumour metastases, (C) particularly breast and prostate cancer, cachexia and anorexia, (C) particularly breast and prostate cancer, cachexia and anorexia, (C) osteopenia, including various forms of osteoporosis, Paget's disease of (C) bone, osteomyelitis, osteonecrosis or bone cell death, associated with (C) traumatic injury or nontraumatic necrosis associated with Gaucher's (C) disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid (C) arthritis, periodontal disease and alopecia. PTH receptor agonists are (C) useful as therapeutic agents in conditions including fracture repair (including healing of non-union fractures), osteopenia, including various forms of osteoperias. AAU73018-AAU73181 represent parathyroid hormone conditions including tracture and (C) and parathyroid hormone related protein (PTH/PTHrP) modulators and (C) related amino acid sequences of the invention
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                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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28-JUN-2000; 2000US-0214860P.
06-FEB-2001; 2001US-0266673P.
26-APR-2001; 2001US-00843221.
   ABJ38267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition, useful for treating osteopenia, comprises parathyroid hormone and parathyroid hormone-related protein receptor modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 AA;
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 standard; protein; 228
                                                                                                                SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                                                                                                                                                                                                      KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
                                                                                                                                                                                                                                        DGVEVHNAKTKPRBEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
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                                                                                           SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
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Pred. No. 4.6e-90;
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Best Local S
Matches 228
                                                                                                                                                                                                                         TALL-1-binding protein; TALL-1; B-cell-mediated autoimmune systemic lupus erythematosus; B-cell-mediated cancer; lympinflammation; rheumatoid arthritis; acute pancreatitis; at
                                                                                                                                                                                                                                                                                                                                                                                          New TALL-1-binding polypeptide, useful for modulating the activity TALL-1 and in treating, preventing or diagnosing a B-cell-mediated autoimmune diseases, cancers or lymphomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multiple myeloma; multiple sclerosis; Parkinson's gene therapy; human IgGlFc; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis; glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                        Claim 36; Fig 3; 236pp; English
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAY-2001; 2001US-0290196P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-MAY-2002; 2002WO-US015273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      АВЈ38267;
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)B; ABT33856.
181
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                                                                                                                                                                        Similarity
           SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                    KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
                                                                                           DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                    MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                        KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
                                                                                 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                        MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                                                                                                                                                                Conservative
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                                                                                                                                                                       100.0%;
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                                                                                                                                                              Score 1238; DB 6;
Pred. No. 4.6e-90;
; Mismatches 0;
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                                                                                                                                                                                  Length
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RESULT 11
ADN59683
ID NADN59
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XX ADN59
XX ADN59
XX ADN59
XX Human
XX Human
XX Human
XX Homo
XX
                                                                                   The invention relates to a thrombopoistin mimetic peptide (TWP) (I) that CC binds to the c-mpl (mpl) receptor, and which stimulates the production of platelet precursors, is new Further CC disclosed is a composition of matter (II) that binds to an mpl receptor, and a pharmaceutical composition comprising (II) and a carrier. The CC pharmaceutical composition of the invention is useful for treating CC thrombocytopaenia in an animal, and for increasing megakaryocytes or CC platelets in a patient. The TWP of the invention is useful for treating CC conditions involving a megakaryocyte and/or platelet deficiency, e.g. CC disease conditions involving thrombocytopaenia such as aplastic anaemia, CC autoimmune tharombocytopaenia, Hughe's syndrome and lupoid thrombocytopaenia. The TWP of the invention is also useful for megakaryocytes and its derived cells. The compounds demonstrate an improved ability to bind to and/or trigger transmembrane signal through, i.e. activating, the mpl receptor the compounds have superior thrombopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryotypopietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryotypopietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryotypopietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of the compounds also exhibit superior therapeutic properties, such as improved plasma half-life, biological activity and in vivo circulation time. The current sequence represents the human IgGl Fc protein that may be used as a preferred represents the human IgGl Fc protein that may be used as a preferred represents.
Sequence
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10-OCT-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADN59683 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thrombopoietin mimetic peptides which bind to mpl receptor, stimulate the production of platelets and/or the production identify the production the production is the procursors, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2003-403101/38
)B; ADN59682.
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2002US-00269806.
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and

Query Match Best Local Similarity

100 . 0%;

Score Pred.

1238; DB 7; No. 4.6e-90;

Length

The present invention describes a peptide (I) that is capable of modulating nerve growth factor (NGF) activity. Also described: (1) modified peptide (II) comprising (I) and a vehicle, where the modified peptide is capable of modulating NGF activity; (2) dimer or multimer of (I); (3) modified peptide (III), its multimers or its salt, where the

of f

Claim

16;

SEQ

ij ö

60; 267pp; English.

Novel peptide capable of modulating nerve for treating disease or disorder e.g., acu

collagen

vascular

disease.

acute

growth factor activity, useful ute pain, dental pain, cancer,

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RESULT 12
ADM17708
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  N-PSDB;
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                                                                                                                    (AMGE-) AMGEN
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18-SEP-2003; 2003US-00666480
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2004-283150/26
DB; ADM17707.
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                                                                     wild KD,
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RESULT 13
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DT 07-OC
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DE Humar
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KW parat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 skin complaints with inflammatory components, sunburn, carditis, dermatitis, myositis, neuritis, collagen vascular diseases, chronic
                                            Homo sapiens
                                                                                                                     osteopathic; osteopenia; IgG
                                                                                                                                                                 parathyroid
                                                                                                                                                                                                                                          Human IgG1
                                                                                                                                                                                                                                                                                                                      07-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADQ75329 standard;
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(6) host cell (VI) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide is capable of modulating NGF activity; (4) polynucleotide encoding (I), (II) or (III); (5) expression vector (V) comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
                                                                                                                                                                                                                                      Fc protein
                                                                                                                     hormone; parathyroid hormone-related protein; PTH; PTHrP; osteopenia; IgG Fc; antibody.
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Pred. No. 4.6e-90;
Mismatches 0;
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WO200024782-A2 Synthetic chrombosis;

matrix metalloproteinase; asthma;

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RESULT 14
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a composition comprising the formula (I): (I) P1 - (L1)a-F1, where F1 = a vehicle and is attached at the C-terminus of P1- (L1)a or through a sidechain at any residue from residue 14 through the C - terminal residue; P1 = a parathyroid hormone/parathyroid hormone-related protein (PTH/PTHFP) modulating domain; L1 is a linker; and a = 0 or 1. The composition of matter is useful for treating osteopenia. This sequence corresponds to a human IgG Fc used in the invention.
                                                                                      Modified peptide; therapeutic agent; fusion; Pc domain; cancer autoimmune disease; cyrostatic; antiasthatic; thrombolytic; Viamunosuppressive; EPO; TPO; CTLA; tinatcic; II-1; TNF; antago; inhibitor; erythropoietin; thrombopoietin; interleukin ; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; vascular endothelial growth factor; matrix metalloproteinase; vascular endothelial growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition of matter comprising parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP) modulating domain and a vehicle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-2002; 2002WO-US036419
                                                                                                                                                                                                          Fc-MMP inhibitor
                                                                                                                                                                                                                                        31-OCT-2000
                                                                                                                                                                                                                                                                        AAB17957;
                                                                                                                                                                                                                                                                                                       AAB17957 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 3A-C; 132pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-2002; 2002WO-US036419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        multimers, useful for treating osteopenia.
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Pred. No. 4.6e-90;
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                                                                                                                                                         c domain; cancer;
thrombolytic; VEGF;
                                                                                                                                                                                                        NO:1068
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                                                                                                                                         antagonist;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes composition of matter (I) comprising an CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, CC P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, CC c, d, e, and f = are each independently 0 or 1, provided that at least 1 CC of a and b is 1. The composition can have cytostatic, antiasthmatic, CC thrombolytic and immunosuppressive activities. DNAs, vectors and host CC compositions. The compositions are useful for treating cancer, asthma, CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions CC such as Fc receptor binding, protein A binding, complement fixation, and CC possibly placental transfer. AAA69443 to AAA69526 and ABB16955 to CAAB18003 represent nucleotide and amino acid sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Sim:
Matches 228;
                                      Fc-MMP inhibitor fusion nucleic acid SEQ ID NO:1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           composition of matter comprising an Fc domain and pharmacologically peptides, useful for treating cancer and autoimmune diseases.
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                                                                                                                              standard; protein; 243
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                                                                                                                                                                                                                          SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                                                                                                                                                                                                                                                                                              KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
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99US-00428082.
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100.0%; Pr
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Modified peptide; mimetic; Fc domain; fusion; immunoglobulin erythropoietin; TPO; tumour necrosis factor alpha inhibitor;

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KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD

DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA

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The present invention describes a vehicle-peptide molecule (I) or its cmultimers. (I) can have antiinflammatory, antitumour, immunosuppressive, cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological, antianaemic, antirheumatic, antiarthritic, antidiabetic, ophthalmological, can antiaremic, antiaremic, antiaremic, ophthalmological, antianaemic, anorectic, antiinferrility, haemostatic, dermatological and comeuroprotective activities. (I) can be used as therapeutic or cytostated proteins of a sease scharacterised by dysfunction of their associated protein of interest, for identifying normal purposes. (I) is useful for their associated composes of interest, as a part of diagnostic kit to detect the presence of their cytoteins of interest in a biological sample. Additionally, (I) is useful for treating inflammatory and autoimmune diseases, tumour growth, cancer, composed arthritis, diabetic retinopathy, obestly, sleep disorders, composed arthritis, diabetic retinopathy, obestly, sleep disorders, commettic compounds are useful for treating disorders characterised by low cred blood cell levels such as anaemia. The TPO-mimetic comprising EPO-mimetic compounds are useful for treating conditions that involve an existing compounds are useful for treating conditions that involve an existing deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic cumour which result in thrombocytopaenia, splastic anaemia, metastatic composed and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777 crepresent maino acid and nucleic acid sequences used in the
                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 228
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-MAY-2000; 2000US-00563286
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DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
                                                                                                        MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                                                                                                                                             MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
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181 SDGSFFILYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228 181 SDGSFFILYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228 181 SDGSFFILYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228 spleted: April 4, 2006, 13:07:40	121 KGOPREDOVYTT. DEGENERITEKNOVST. TOT VKGEYDSOT AVEWESING DENNYKTTTODVT. D. 180

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Minimum DB seq length: 0
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Listing first 45 summaries
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PIR 80:*
1: pir1:*
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1238
1 MDKTHTCPPCPAPELLGGPS.....MHEALHNHYTQKSLSLSPGK 228
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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_	gamma-2a		gamma-1	gamma-1 chain	chain	noclonal antibo	gamma-3 c		gamma-3	gamma-1 chain	heavy chain C	heavy chain pr	gamma 3 chain	gamma 1 chain	gamma-2	gamma 4 chain	gamma 2a	gamma 2b cha	chain C	gamma-3 heavy	4	gamma-2 chain	-3 chain	gamma-3 chain	gamma chain C	chain V	gamma-1 cha	gamma-1 chain	Description	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
357.5	358	358	395.5	571	574.5	577.5	707	757	764	774	779	785.5	794	802	804
28.9	28.9	28.9	31.9	46.1	46.4	46.6	57.1	61.1	61.7	62.5	62.9	63.4	64.1	64.8	64.9
549	453	343	572	152	218	249	180	475	327	405	474	322	446	335	399
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S04845	S37768	S25644	B46529	S14236	A36040	S69340	I46732	S01321	S06611	G2MSBM	G2MS11	PS0019	S40295	G2MSAB	G2MSAM
Ig heavy chain pre	Ig mu chain C regi	mu chain	_	Ig gamma-1 chain (•	heavy	_	gamma-2b	gamma-2 c	Ig gamma-2b chain	Ig gamma-2b chain	gamma-2a	gamma-2a		gamma-2a

ALIGNMENTS

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A; Residues: 88-113;235-330 <TAK>
A; Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:Z17370
R; Cunningham, B.A; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Ede
Biochemistry 9, 3161-3170, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid
A; Reference number: A90563; MUID:71064024; PMID:5489771
A; Contents: myeloma protein Eu
A; Accession: B90563
A; Molecule type: protein
A; Residues: 1-96, 7*, 98-135 <CUN>
A; Cross-references: UNIPARC:UPI000017378D
A; Cross-references: UNIPARC:UPI000017378D
A; Note: this sequence has the Gim(3) maxker, 97-Arg
R; Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid
A; Accession: A90564; MUID:71064025; PMID:5530842
A; Molecule transporters
                                                       A;Molecule type: protein

A;Molecule type: protein

A;Residues: 1-96,'R', 98-197,'D',199-238,'E',240,'M',242-266,'D',268

A;Cross-references: UNIPARC:UPI0000173790

A;Note: this sequence has the GIm(3) and GIm(non-1) markers

R;Gall, W.B.; Edelman, G.M.

Biochemistry 9, 3188-3196, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. X

A;Reference number: A90565; MUID:71064027; PMID:4923144

A;Contents: annotation; disulfide bonds

R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976

A;Title: Rule of antibody structure. The primary structure of monocal products, and the disulfide bridges.

A;Reference number: A91667; MUID:77070267; PMID:1002129

A;Contents: annotation; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-330 <ELL>
A;Cross-references: UNIPROT:PO
A;Note: this sequence has the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: this sequence has the Glm(17) and Glm(1) markers R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N. Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983 A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen A;Reference number: A91723; MUID:83289131; PMID:6884994 A;Contents: myeloma protein KOL; disulfide bonds A;Accession: A91723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A;Residues: UNIPARC:UPI000017378E
A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
A;Ponstingl, H.; Hilschmann, N.
H;Ponstingl, H.; Hilschmann, N.
Hoppe-Seylee's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Structure of human immunoglobulin A;Reference number: S33887; MUID:83001943; A;Accession: S33887 A;Molecule type: DNA
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A;Molecule type: DNA
A;Residues: 2-330 <HAR>
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A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Cross-references: UNIPARC:UPI000017378F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Contents: myeloma protein
A;Accession: B91668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A91668; MUID: 77070269; PMID: 826475
A;Gene:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370 Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the
                                    ;Contents: annotation;
;Genetics:
       GDB: IGHG:
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PMID:6811139
                                                                                                                                                                                                                                                                                                                      gammaG-immunoglobulin.
PMID:4923144
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                                                                                                                                                                                 monoclonal
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A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14032.33-14032.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IQA and IgM, the subunits associate int c;Superfamily: immunoglobulin cregion, immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C;Superfamily: immunoglobulin homology C]Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology <IMI>
F;20-85/Domain: immunoglobulin homology <IMI>
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F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,550-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region precursor - human (;Species: Homo sapiens (man) (;C;Species: Homo sapiens (man) (;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000 (;Accession: S69339; S72664 R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
S69339
                                                                                                                                                                                                                                                                                                                                                                                                           R;Khamlichi, A.A.
submitted to the EMBL Data Library,
A;Reference number: $72664
A;Accession: $72664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition
A;Reference number: S69339; MUID:95262687; PMID:7744049
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A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: UNIPARC:UP10000176F25; EMBL:X81695
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                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
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Best Local
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227; Conserv
208
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GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
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                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                   99.1%;
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100.0%; Pred. No. 7.9e-89;
tive 0; Mismatches 0;
                                                                                                                                                                                               2
                                                                                                                                                                                                                      Score 1227; DB 2;
Pred. No. 2.7e-88;
                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                DB 2;
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                                                                                                                                                                                                                                          Length 374;
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Ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-
C;Accession: PT0207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc
A;Reference number: PT0207; MUID:91287716; PM:
A;Accession: PT0207
A;Molecule type: mRNA
A;Residues: 1-234 <EHR>
A;Cross-references: UNIPARC:UPI0000176F05
C;Superfamily: immunoglobulin C region; immunn
C;Keywords: immunoglobulin homology <IMM.
F;48-117/Domain: immunoglobulin homology <IMM.
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                                                                       A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglob
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain A;Reference number: A23511; MUID:86148507; PMID:3081877
                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-377 < HUC>
                                                                                                                                                                                                                                                                                                                                             R; Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc,
                                                                                                                                                                                                                                                                                                                                                                 Ig gamma-3 chain C region (allotype G3m(b)) - human C;Species: Homo sapiens (man) C;Deceies: Homo sapiens (man) C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change C;Accession: A23511
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Best Local Similarity
Matches 217; Conserv
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                                                       immunoglobulin homology <IMM>
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ilarity 98.6%;
Conservative
   92
92
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 Score
Pred.
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1146; DB 2;
No. 5.7e-82;
                                                                                             immunoglobulin
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PMID:2062315
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A; Molecule type: DNA A; Residues: 1-326 <ELL> A; Cross-references: UNI

UNIPROT: P01859; UNIPARC: UPI000003BFCC; GB: V00554;

GB:J00230;

immunoglobulin

gamma

heavy

chain

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09-Jul-2004

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Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change
C;Date: 30-Apr-1980 #sequence revision 13-Jun-1983 #text_change
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobul
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
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A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:Q8N4Y9; UNIPARC:UPI0000176F0B
C;Superfamily: immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, A;Reference number: A60764; MUID:90007613; PMID:2571587 A;Accession: A60764
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Huck, S.; Lefranc, G.; Lefranc, Immunogenetics 30, 250-257, 1989 A;Title: A human immunoglobulin IC
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C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision
C;Accession: A60764
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Best Local Similarity
Matches 210; Conserv
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Pred. No. 8
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A;Note: Lys-326 is probably removed posttranslationally R;Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: gel A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A;Cross-references: UNIPARC:UPI0000173791
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Blochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain cons A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Cross-Leveller, D.M.
R; Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A; Reference number: A94591
A; Contents: annotation; Zie, revisions to
A; Contents: annotation; Zie, revisions to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Milstein, C.; Frangione, B.
Blochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human A;Title: Disulphide bridges of the heavy chain of human A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bo R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Wature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: A note on the amino acid sequence of residues 381-391
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Contents: N93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
A;Cross-references: UNIPARC:UPI0000173794
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A;Molecule type: protein
A;Residues: 1-24,'E', 26-57,'EV', 60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-A;Residues: UNIPARC: UPI0000173792; UNIPARC: UPI0000173793
A;Cross-references: UNIPARC: UPI0000173792; UNIPARC: UPI0000173793
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol 16, 923-925, 1979
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A;Map position: 14432.33-14432.33

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light C;Complex: An immunoglobulin heterotetramer grand IgM, the subunits associate int hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology <IMIX
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,133-202/Domain: immunoglobulin homology <IM2>
,239-306/Domain: immunoglobulin homology <IM3>
,239-306/Domain: immunoglobulin homology <IM3>
,239-306/Domain: immunoglobulin homology <IM3>
,14/Disulfide bonds: interchain (to light chain) #status experimental
,27-83,140-200,246-304/Disulfide bonds: #status experimental
,27-83,140-200,246-304/Disulfide bonds: interchain (to heavy chain) #status
,102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status
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  165
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                                      NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
                                                                                                                CPPCPAPP-VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVH
                                                                                                                                                                   CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHBDPEVKFNWYVDGVEVH
                                                                                                                                                                                                                                                            92.3%;
94.1%;
                                                                                                                                                                                                                              Score 1142.5; DB 1;
Pred. No. 8.9e-82;
8; Mismatches 4;
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that shown i
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A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Residues: 1-327 <ELL>
A;Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190
A;Ote: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C
Blochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses: Partial amino a
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
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C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982
C;Accession: A90933; A90249; A02150
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A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
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A;Residues: 1-30;81-326 <PIN>
A;Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796
C;Genetics:
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DNA 1, 11-18, 1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;140/Disulfide bonds: interchain (to light chain) #status experimental F;27-83,141-201,247-305/Disulfide bonds: #status predicted F;27-83,141-201,247-305/Disulfide bonds: #status predicted F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental files of the control of the 
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                                                                                                                                                                                                                                                                                                                                                                                     NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 126
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                                                                                                                                                                                                                  PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
                                                                               LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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93.7%;
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Pred. No. 3.4e-81;
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PMID:4192699
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Milstein, C.
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G3HUWI

G3HUWI

G3HUWI

G gamma-3 heavy chain disease proteins - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1979 #sequence revision 23-Oct-1981 #text_change 16-Jul-1999

R;Prangione, B.; Prangione, B.; Franklin, E.C.

A;Cocsesion: A90442; MUID:81021548; PMID:6774747

A;Contents: heavy chain disease protein Wis

A;Accession: A90442

A;Molecule type: protein

A;Rote: the sequence: UNIPARC:UPI0000173797

A;Cocsesidues: 1-289-cFRA-

A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain A;Note: the sequence of residues 42-76 was taken from the reference that follows

R;Michaelsen, T.E.; Frangione, B.; Franklin, E.C.

J. Biol. Chem. 252, 883-889, 1977

A. Fills: Primary etruncture of the 'hinge' region of human IGG3. Probable quadruplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-157
A;Cross-references: UNIPARC:UPI000017379A; UNIPARC:UPI000017379B; UNIPARC:UPI000017379C;
A;Note: a carboxyl-terminal Lys is removed posttranslationally
A;Note: this sequence may represent an allelic form or another gamma chain subclass
C;Comment: The heavy chain disease protein Wis is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C. Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein A;Reference number: A90198; MUID:77021516; PMID:823945
A;Contents: heavy chain disease protein Zuc, partial sequence corr
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                                                                                                                                                                                                                                                                                                                                  F;1/Modified site: F;6,140/Binding sit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: this protein lacks most of the V region, all of the R; Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A; Title: gamma heavy chain disease in man: cDNA sequence su A; Reference number: A93915; MUID:82247835; PMID:6808505
A; Contents: heavy chain disease protein Omm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Primary structure of the 'hinge' region of human A;Reference number: A92219; MUID:77118561; PMID:402363 A;Contents: normal gamma-3 chains, sequence corresponding A;Accession: A92219
  밁
                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: duplication; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: immunoglobulin C region; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: GDB:IGHG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A93915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
A; Cross-references: UNIDARC: UPI00001,73799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UPI0000173798
A;Note: the hinge region in gamma-3 chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 12-97 < MIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A90198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             idue segment (12-28)
                                                                                                                                                                                                                     Query Match
Best Local S
Matches 204
                                                                                                                                                                                                                                                                                                                                  Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid; 203-270/Domain: immunoglobulin homology <IMM>.
;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
124
                                                     62
                                                                                                          64
                                                                                                                                                                                                                                                  Similarity
                                                  GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
                                                                                                                                        DKTHTCPPCPAPELLGGPSVFLFPPKFXDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                               90.5%;
                                                                                                                                                                                                            Score 1121; un
Pred. No. 3.6e
13; Mismatches
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pyroglutamic acid
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A;Cross-references: UNIPROT:P01870; UNIPARC:UPI000012B37D
A;Note: this sequence has the d12 allotypic marker; 104-Thr, and i
R;Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A;Title: Sequence studies on the constant region of the Fd section
A;Reference number: A90290; MUID:76135469; PMID:1243651
A;Accession: A90290
A;Molecule type: protein
A;Residues: 1-47'E,49-71',PV',72-128 <PRA>
A;Cross-references: UNIPARC:UPI0001737AB
R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.I
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A;Title: Heavy chain genes of rabbit IGG; isolation of a cDNA ence
A;Reference number: A9328; MUID:8329917; PMID:6193512
A;Accession: A9328
                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Molecule type: protein
A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q'
A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q'
A;Cross-references: UNIFARC:UPI00001737AD; UNIFARC:UPI00001737AE
A;Note: this has the e15 allotypic marker, 185-Ala
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k.
C;Complex: An immunoglobulin heterotetramer subunit sassociate into
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin credion; heterotetramer; immunoglobulin
C;Reywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C;Reywords: immunoglobulin homology <IMI>
F;20-82/Domain: immunoglobulin homology <IMI
F;20-82/Domain: immunoglobulin 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 88-103; M',105-143,'E',145-184,'A',186,'E',188-266 <MAR>
A;Residues: 88-103; M',105-143,'E',145-184,'A',186,'E',188-266 <MAR>
A;Cross-references: UNIPARC:UPI000016C5ED; GB:M16426; NID:g165111; PIDN:AAA31289.1;
A;Note: this sequence has the dii allotypic marker, 104-Met, and the e15 allotypic m R;Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A;Tille: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobu A;Reference number: A90245; MUID:70110015; PMID:5461106
A;Accession: A90245
        엉
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A;Residues: 132-143, 'E',145-161 <FRU's
A;Cross-references: ULPI00001737AC
A;Hll, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp. A;Reference number: A94416
A;Accession: A94416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Nucleotide sequence of a rabbit IgG heavy chain A;Reference number: A91749; MUID:84030930; PMID:6313520 A;Accession: A91749
A;Molecule type: mRNA
A;Residues: 1-323 <BER>
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C;Date: 24-Apr-1984 #sequence revision 15-Nov-1984 #t
C;Accession: A91749; A90290; A9928; A90245; A94416;
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
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GHRB
                                                                                                                                                                                                                                                                                                        F;173/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                F;130-199/Domain: immunoglobulin homology <IM2>F;236-303/Domain: immunoglobulin homology <IM3>
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Species: Oryo
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        91
                                                                                                                                                        ll Similarity
DGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                        Score 918.5;
Pred. No. 2.6
                                                                                                                                                                                                                                                                                                        (covalent)
                                                                                                                                                                                            .6e-64;
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6; A02161
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RESULT 11
147160
Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_ch
C;Accession: I47160
R;Kacskovics, I; Sun, J; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified f
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mENA
A;Residues: 1-328 <KAC>
A;Cross-references: UNIPARC:UPI0000115525; EMBL:U03780; NID
C;Genetics:
A;Gene: IgG2b
C;Superfamily: immunoglobulin C region; immunoglobulin homo
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                           RESULT 12
147159
19 gamma 2a chain constant region - pig (C;Species: Sus scrofa domestica (domestic C;Date: 21-Feb-1997 #sequence revision 21 C;Accession: 147159
R;Kacskovics, I; Sun, J; Butler, J.E. J. Immunol. 153, 3565-3573, 1994
C; Genetics:
A; Gene: IgG2a
C; Superfamily:
                                                   A;Title: Five putative subclasses of swine IgG identific A;Reference number: I47158; MUID:95015845; PMID:7930579 A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-328 <KAC>
A;Cross-references: UNIPARC:UPI0000115524; EMBL:U03779;
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                                                                                                                                                                                                                g gamma 2a chain constant region - pig (fragment); Species: Sus scrofa domestica (domestic pig)
Date: 21-Feb-1997 #sequence_revision 21-Feb-1997; Accession: 147159
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CPICPACE-SPGPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISKARGOPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTT
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                                                                                                                                                                                                                                                                                                                                                           YFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTQKSISKTPGK
   immunoglobulin
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 region;
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   immunoglobulin homology
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                                                        PIDN: AAA52217.1;
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 Ig gamma-2 chain C region - guinea pig (;Species: Cavia porcellus (guinea pig) C;Date: 07-May-1981 #sequence revision: C;Accession: A94553; A90352; Ā90359; A9 R;Trischmann, T.M. submitted to the Atlas, April 1975 A;Reference number: A94553
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on 07-May-1981 #text_change A90384; A90385; A02151

09-Jul-2004

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RESULT 13
147162
Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997
C;Accession: 147162
R;Kacskovics, I.; Sun, J.; Butler, J.E.
                                                                                                                                                                                                                                                                                                                                                    A;Gene: IGG4
C;Superfamily: in
F;82-151/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A; Title: Five putative subclasses of swine
A; Reference number: 147158; MUID:95015845;
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-277 < KAC>
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                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: UNIPARC: UPI0000115527;
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Best Local S
Matches 167
                                                                                                                                                                                                                                                                                                                                                      Superfamily: immunoglobulin C;82-151/Domain: immunoglobulin
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Best Local
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223
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                                                                  TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYK
                                                                                                                                                                                                                                                 MDK---THTCPPCP-APELLG-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 55
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                TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                                                                                                                                        FSWYVDGVEVHTAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITR
                                                                                                                                                        FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK
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TTPPQQDVDGTYFLYSKLAVDKASWQRGDTFQCAVMHEALHNHYTQKSIFKTPGK
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73.2%;
                                                                                                                                                                                                                                                                                73.0%; Score 903.5;
71.1%; Pred. No. 3.20
Live 30; Mismatches
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                                                                                                                                                                                                                                                                                                                                                      region; immunoglobulin
homology <IMM>
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Pred. No. 2.
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A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A;Reference number: A90354; MUID:71058474; PMID:492544
A;Rontente: annotation; disulfide bonds
A;Note: Cys-16 is involved in a heavy-light chain bond
A;Note: Cys-105; Cys-107, and Cys-110 form inter-heavy chain bonds
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1:
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R;Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2).
A;Reference number: A90359; MUID:71058486; PMID:5538616
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F;241-310/Domain: immunoglobulin homology <IM3>
F;28-79/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 227-311 <TR2>
A; Cross-references: UNIPARC: UPI00001737A3
R; Oliveira, B; Lamm, M.E.
Biochemistry 10, 26-31, 1971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UPI00001737A2
R;Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A;Reference number: A90385; MUID:75036073; PMID:4609467
A;Accession: A90385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
B;Title: Primary structure of the C-H2 homology region from A;Reference number: A90384; MUID:75036072; PMID:4429665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 69-133;312-329 <TUR>
A;Cross-references: UNIPARC:UPI00001737A0; UNIPARC:UPI00001737A1
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A;Accession: A90352
A;Molecule type: protein
A;Residues: 4-68 <BIR>
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A;Molecule type: protein
A;Residues: 1-3 <TRI>A;Crose-references: UNIPROT:P01862; UNIPARC:UPI000017379E
R;Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
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Best Local
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SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                          GNAETKPRVEQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPR
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                                                                                                                                                                                                                                                                                                                                   TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 65
                                                      MPDVYTLPPSRDELSKSKVSVTCL1INFFPADIHVEWASNRVPVSEKEYKNTPP1EDADG
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72.3%;
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MUID:71058471; PMID:5538606
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Pred. No. 5.3e-62;
4; Mismatches 36
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Search completed: April Job time: 37.3037 secs

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Ig gamma 1 chain cons C;Species: Sus scrofs C;Date: 21-Feb-1997 + C;Accession: 147158 R;Kacskovics, I.; Sur J. Immunol. 153, 3569

chain constant region - pig (fragment)
Sus scrofa domestica (domestic pig)
-Feb-1997 #sequence_revision 21-Feb-1997

#text_change 21-Jan-2000

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J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47158
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KACC>
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C;Superfamily: immunoglobulin C region; immunog
F;133-202/Domain:'immunoglobulin homology <IMM>
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Matches 163;
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                                                                                                                                                                         66 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 125
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TFFLYSKLAVDKARWDHGDKFECAVMHEALHNHYTQKSISKTQGK 328
                             SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                           EPQVYTLPPPAEELSRSKVTLTCLVIGFYPPDIHVEWKSNGQPEPENTYRTTPPQQDVDG
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ive 27; Mismatches
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Match
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1 MDKTHTCPPCPAPELLGGPS.....MHEALHNHYTQKSLSLSPGK 228
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Q6GNX6 HUMAN
Q6GNX7 HUMAN
Q727P5 HUMAN
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	crystallized	HD.,	PubMed=6	hyŝic	hain, omple	dy at (mye	chmann 1	EQUENCE (MYELOMA PR	1-3181 (19		Cunningham	F 136-3;	.61-3170 (19	structure of	.A., Rutishauser	F 1-135	es. 10:4071-	rson B.J., sequence of	g. PubMe		n). ; Chordata; ; Euarchont	region	, Las	Cre	TANDARD;		29 70	337 329	23	0 6	70	27 73	654	21
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	obulin 1	HD., Palm W., Hilschmann N.; structure determination of antibodi), AND DISULFIDE	571-1604 (1976)	he tryptic pep	primary structure Nie). III. The ch		3).		gamma G-immunoglobul	ett C., Konigsbe		n promine tragment	_	l W.E., Gottlieb P	PROTEIN EU).		immunoqlobulin C q			ta; Vertebrata; Eu; Primates; Catarı		update)		330 AA.	MENTS								
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GO; GO:0005624; C:membrane fraction; NAS.
GO; GO:0003823; F:antigen binding; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR0031097; Ig-like.
InterPro; IPR0030597; Ig_cl.
InterPro; IPR0030597; Ig_MHC.
Pfam; PP07654; Cl-set; 3.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS50835; IG_MHC; 2.
PROSITE; PS00299; IG_MHC; 2.
PROSITE; Direct protein sequencing; Glycoprotein; Immunoglobulin C region; Immunoglobulin domain.
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#Peker L., Schwarz J., Reichel W., Hilschmann N.; 

#Pule of antibody structure. The primary structure of a monoclonal 

19G1 immunoglobulin (myeloma protein Nie), I: purification and 

characterization of the protein, the L- and H-chains, the cyanogen 

bromide cleavage products, and the disulfide bridges."; 

Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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Gall W.E., Edelman G.M.;
"The covalent structure of a human
Intrachain disulfide bonds.";
Riochemistry 9:3188-3196(1970).
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MISCELLANEOUS: Nie also differs in the amidation state 116, 198, 269 and 272.
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; A/B=106-330.
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/FTId=VAR 003886.
D -> E (in GlM(non-1) marker).
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L -> M (in GlM(non-1) marker).
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RP TISSUE=Primary B-Cells;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altachen R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altachen R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Gadin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Stapleton M., Gudin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Robards S., Morley R.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Morley R.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Va Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Pahey J., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Va Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human
EMBL; BC073766; AAH73766.1; -; mRNA;
GO; GO:0016021; C:integral to membrane; IE
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.C1.
InterPro; IPR003597; Ig.C1.
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PROSITE; PS00835; IG LIKE; 4.
PROSITE; PS00835; IG LIKE; 4.
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Hypothetical protein.
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05-JUL-2004 (TrEMBLrel. 27,
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RC TISSUE-Peripheral Nervous System;
RC TISSUE-Peripheral Nervous System;
RX MEDLINE-22388257; pubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet Z T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Halesley A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Grimpus CDNA sequences.";
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Best/Local S
Matches 227
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig c1.
InterPro; IPR003596; Ig MHC.
InterPro; IPR003596; Ig v.
Pfam; PF07654; C1-set; 3.
                                                                                              Submitted (JUN-200
EMBL; BC072419; AA)
HSSP; P01861; 1ADQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Homin
                                                                                                                                                              NUCLEOTIDE SEQUENCE.
TISSUE=Peripheral Nervous System;
                                                                                                                                                  NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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Name=IGHG1;
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_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239
                                                                                                               tted (JUN-2004) to the EMBL/GenBank/DDBJ BC072419; AAH72419.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
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27,
27,
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Last sequence update)
Last annotation update)
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Pred. No. 9e-92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              466
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Q569F4 HUMAN
ID Q569F4 H
AC G569F4 H
AC G569F4 H
AC MEDLINE-
RA Klausnes
RA RA Raha S. S.
RA Bosak S. S.

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Best Local S
Matches 227
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SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv.1; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN
SEQUENCE 466 AA; 50854 MW; 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q569F4_HUMAN
Q569F4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGHG1 protein.
Name=IGHG1;
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10-MAY-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-2005
      Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases. EMBL; BC092518; AAH92518.1; -; mRNA. SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;
                                                                                                                                                         NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.6%;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsish F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci p., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci p., Prange C.,

RA Barownstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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"Generation and initial analysis of more than 15,000 full-length human

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Best Local Similarity
Submitted (APR-2003) to the EMI EMBL; BC051328; AAH51328.1; -; HSSP; P01857; 1HZH. SMR; Q7Z7P5; 20-469. InterPro; IPR007110; Ig-like. InterPro; IPR003597; Ig_cl. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_WhC. InterPro; IPR003596; Ig_V. Pfam; PF07654; C1-set; 3.
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Euarchontoglires, Primates, Catarrhini, Hominidae,
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Pred. No. 9.1e-92;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Roha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.;
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Warra M.A.;
"Generation and initial analysis of more than 15,000 full-length human RI and mouse cDNA sequences.";
RI Proc. Natl. Agad. Sci. U.S. A. 9416899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
Q7Z5W1_HUMAN
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Best Local Sim
Matches 227;
         EMBL; BC053984; AAH53984.1;
EMBL; BC053987; 1HZH.
HSSP; P01857; 1HZH.
InterPro; IPR007110; Ig-lik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                 Strausberg R.;
                                                                                                      TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7Z5W1_HUMAN
Q7Z5W1;
                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                                                                     (JUN-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               469 AA;
                                                                                                                                                          Acad.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                         U.S.A. 99:16899-16903(2002)
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26,
                                                                  the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
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Pred. No. 9.1e-92;
                                                   mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                         15,000 full-length human
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RESULTATION OF THE CONTROL OF THE CO
                                                                                                                                                                        RC TISSUE-Primary B-Cells;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Rahas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rahas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S.M., McEwan N., Madan A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human

"T and mouse CDNA secondary "."
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Best Local S
Matches 227
TISSUE=Primary B-Cells;
NIH MGC Project;
Submitted (DEC-2001) to
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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InterPro; IPR003596; Ig_v.
Pfam; PF07654; CI-set; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_MHC; UNKNOWN 2.
PROSITE; PS00290; IG_MHC; UNKNOWN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6PJA4_HUMAN
Q6PJA4;
                                                                                     NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                       cDNA sequences."
l. Acad. Sci. U.S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Homin
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                                                                                                                                          U.S.A.
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27,
27,
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Last annotation update)
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Pred. No.
                                                                                                                                       99:16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₿
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EMBL/GenBank/DDBJ databases

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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR00359; Ig.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; Cl-set; 3.
SMART; SM00407; IGcl; 3.
SMART; SM00407; IGcl; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_MHC; UNKNOWN 2.
SEQUENCE 470 AA; 51716 MM; 7B495
                                       Interpro; IPR003539; Ig.
Interpro; IPR007110; Ig-like.
Interpro; IPR003197; Ig-cl.
Interpro; IPR003597; Ig-cl.
Interpro; IPR003906; Ig-MHC.
Interpro; IPR003906; Ig-MHC.
Interpro; IPR003906; Ig-y.
Pfam; PF07654; Cl-set; 3.
SMART; SM00400; IG; 2.
SMART; SM004007; IGcl; 3.
SMART; SM004007; IGcl; 3.
SMART; SM004007; IGCl; 3.
SMART; SM004007; IGCl; 3.
SMART; SM004007; IGCl; 4.
PROSITE; PS00290; IG-MHC; UNKNOWN 2.
                                                                                                                                                                                                                                                                                                                                   TISSUE=Rectum tumor;
The German cDNA Consortium;
The German cDNA Consortium;
Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C.,
Pobo G., Han M., Wiemann S.;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ database
EMBL, B8640627; CAES45781.1; -; mRNA.
HSSP; P01861; IADQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686P15220.
Name=DKFZp686P15220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q6N089;
Q6N089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Sim
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8
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P01861; 1/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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  al protein.
472 AA; 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH18747.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Hominidae;
     51724 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.6%;
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; Pred. No. 9.1e-92;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WN 2.
7B49556A11FD7D99
       26CB340D0046D279 CRC64;
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Best Local S
Matches 227
                                                                                                                                                                                                                 Query Match
Best Local S
Matches 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2005) to the EMBL/GenBank/DDBJ datematic (JAN-2005) to the EMBL/GenBank/DDBJ datematic AY894992; AAW82028.1; -; mRNA.

InterPro; IPR003599; Ig. cl.
InterPro; IPR003597; Ig. cl.
InterPro; IPR003597; Ig. cl.
InterPro; IPR003596; Ig. MHC.
InterPro; IPR003396; Ig. WHC.
InterPro; IPR003396; Ig. v.
Pfam; PF07654; C1-set; 3.
Pfam; PF07654; C1-set; 3.
SMART; SM00406; IG; 1.
SMART; SM00406; IG; 1.
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Q5EFE5;
10-MAY-2005
                                                                                                                                                                                                                                                                                                                                              Signal.
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence determination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IO-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Anti-RhD monoclonal T125 gammal heavy chain precursor.
                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
Gaucher C., Klein P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody T125.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _HUMAN
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                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               PS50835;
PS00290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKTHTCPPCPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                       GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                                                          DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
    GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPBNNYKTTPPVLDS
                                                                                                                                 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                         475
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                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                         ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                           IG_LIKE;
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100.0%; Pr
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475
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                                                                                                                                                                                                                                                                                                         52362 MW;
                                                                                                                                                                                                                                          99.6%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                    UNKNOWN
                                                                                                                                                                                                             0;
                                                                                                                                                                                                                 Score 1233; Db 2; pred. No. 9.3e-92; Pred. No. 9.3e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1233; DB 2;
Pred. No. 9.2e-92;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                          Potential.
anti-RhD monoclonal
chain.
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L. Shemmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L. Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA semences "."
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                                                                                                                                                                                                                                                                                       Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC073782; AAH73782.1; -; mRNA.

GO; GO:0016021; C:integral to membrane; IEA.

R Interpro; IPR003599; Ig.

R Interpro; IPR007110; Ig-like.

R Interpro; IPR003597; Ig. Cl.

R Interpro; IPR003597; Ig. MHC.

R Interpro; IPR003596; Ig. MHC.

R SMART; SM00409; IG.; 2.

R SMART; SM00409; IG.; 3.

R SMART; SM004007; IGC1; 3.

R SMART; SM00406; IGV; 1.

R PROSITE; PS50835; IG_MHC; UNKNOWN_2.
                                                                                                                             Matches
                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                          Hypothetical protein SEQUENCE 475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
Homo sapiens (Human).
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05-JUL-2004
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Q6GMW7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Spleen;
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HUMAN
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   249
                                                             N
                                                                                                                                                      Similarity
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                   DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475
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(TrEMBLrel. 27,
                                                                                                                   99.6%; So ilarity 100.0%; 1 Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
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Last annotation updat
                                                                                                                Score 1233; DB 2;
Pred. No. 9.3e-92;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99:16899-16903 (2002)
                                                                                                                                                                                                                                             2A1FE55D736860F8 CRC64;
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                                                                                             A Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ dat
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ dat
EMBL; BC073773; AAH73773.1; -; mRNA.
GO; GO:0016021; C::Integral to membrane; IEA.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig. cl.
R InterPro; IPR003597; Ig. cl.
R InterPro; IPR003596; Ig_MHC.
R InterPro; IPR003596; Ig_W.
R InterPro; IPR003596; Ig_V.
R Pfam; PP07654; Cl-set; 3.
R SMART; SM00409; IG; 2.
R SMART; SM00409; IG; 2.
R SMART; SM00406; IGV; 1.
R SMART; SM00406; IGV; 1.
R SMART; SM00406; IGV; 1.
R PROSITE; PS00290; IG_MHC; UNGNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R. L., Peingold E.A., Grouse L. H., Derge J. G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K. H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Change C.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and semiences".
   Query Match
                                                             Hypothetical SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel.
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                                                       al protein.
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                                                             52286 MW;
   99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A. 99:16899-16903(2002)
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Last annotation updat
   Score 1233; DB 2;
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                                                             622AABA5C62DDE9D CRC64;
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Length 476;
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                                                                                                                  GO; GO:0006508; P:profecolysis and peptidolysis; IE)
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR00181; EGF_Z.
InterPro; IPR00181; EGF_GA.
InterPro; IPR00181; EGF_IIE.
InterPro; IPR002039; EGF_Iike.
InterPro; IPR002383; EGF_Iike.
InterPro; IPR002383; EGA_blood.
InterPro; IPR007110; Ig_Tike.
InterPro; IPR003397; Ig_C1.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003006; Ig_MCC.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Factor VII active site mutant immunoconjugate.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P08709; iKLI.

SMR; O96PQB; 39-180, 191-444, 447-679.
Ensembl; ENGG0000057593; Homo sapiens.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005599; F:calcium ion binding; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004295; P:proteolysis and peptidolysi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
Hu Z., Garen A.;
Submitted (FEB-2003) to t
EMBL; AF272774; AAK58686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Targeting tissue factor on tumor vascular endothelial cells and cells for immunotherapy in mouse models of prostatic cancer."; Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Euarchontoglires;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q96PQ8_HUMAN
PRINTS; PRO0010; EGFBLOOD.
PRINTS; PR00001; GLABLOOD.
SMART; SM00179; EGF_CA; 1.
                                                            Pfam; PF000008; BGF; 1.
pfam; PF000594; Gla; 1.
pfam; PF000594; Typpsin; 1.
pfam; PF00089; Typpsin; 1.
prints; PR00722; CHYMOTRYPSIN.
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HUMAN
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            RC TISUES-Peripheral Nervous System;
RC MEDLINE-22388257; pubMed=12477932; DOI=10.1073/pnas.242603899;
RX MEDLINE-22388257; pubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carning P. Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carning P. Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Hotterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maxra M.A.;
RA Schnerch A., Schein J.E., Jones S.J.M., Maxra M.A.;
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Best Local S
Matches 227
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PROSITE; PSOULAGE; EGF 3; 1.

PROSITE; PSOULAGE; EGF CA; 1.

PROSITE; PSOULAGE; EGF CA; 1.

PROSITE; PSOULAGE; EGF CA; 1.

PROSITE; PSSOULAGE; ELIKE; 2.

PROSITE; PSSOULAGE; IG_MHC; UNKNOWN_1.

PROSITE; PSSOULAGE; TRYPSIN_DOM; 1.

PROSITE; PSSOULAGE; TRYPSIN_HIS; UNKNOWN PROSITE; PSOULAGE; TRYPSIN_SER; 1.

SEQUENCE 679 AA; 75552 MW; 0B0023A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         055 HUMAN OFFITMINARY;
O6P055 HUMAN PRELIMINARY;
O6P055 O5-JUL-2004 (Trembirel 2
05-JUL-2004 (Trembirel 2
05-JUL-2004 (Trembirel 2
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SMART; SM
SMART; SM
SMART; SM
PROSITE;
PROSITE;
PROSITE;
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Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; El
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM00069; GLA; 1.
SM000407; IGC1; 1.
SM00020; Tryp SPC; 1.
Sp 9800010; ASX HYDROXYL; UNKNOWN 1.
E; PS00022; EGF 1; UNKNOWN 1.
E; PS01186; EGF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GOPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.6%; bu
100.0%; br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27,
27,
27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1233; Db 4;
Pred. No. 1.5e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OB0023AE70A067A1
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      15,000
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        full-length
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        human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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Tobelat

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RESULT 14

Q6MZQ6 HUMAN

ID Q6MZQ6;

AC Q6MZQ6;

DT 05-JUL-2

DT 05-JUL-2

DT 05-JUL-2

DT 05-JUL-2

DT 05-JUL-2

OC HAMMONIA

CE LARYOCKHEE

GN NAME-DKF

OS HOMO SAP

OC EUKARYOT

CH MAMMONIA

CH MAMMONIA

CH TISSUE=E

RG TISSUE=E

RG TISSUE=E

RG THE GATM

RA BAHR A.,

RA BAHR A.,

RA BAHR A.,

RA BAHR A.,

RA BAHR, BX

DR SMR; Q6M

DR InterPro

DR InterPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 226
Han M., Wiemann s.;
Submitted (JAN-2005) to the EMBI
EMBL; BX640947; CAE45972.1; -; |
HSSP, P01861; 1ADQ.
SMR; Q6MZQ6; 20-475.
InterPro; IPR003599; Ig.like.
InterPro; IPR007110; Ig_1like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003599; Ig.
InterPro; IPR00310; Ig-like.
InterPro; IPR003107; Ig-like.
InterPro; IPR003597; Ig-cl.
InterPro; IPR003596; Ig-MHC.
InterPro; IPR003596; Ig-WC.
InterPro; IPR003596; Ig-WC.
InterPro; IPR003596; Ig-WC.
InterPro; IPR003596; Ig-WC.
InterPro; IRR003596; IG-LIKE; IRR03517E; PS50835; IG-LIKE; IRR0517E; PS50835; IG-LIKE; IRR0517E; PS508395; IG-MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06 HUMAN PRELIMINAKY;

06MZ06 HUMAN PRELIMINAKY;

06MZ06;

05-JUL-2004 (TrEMBLrel. 27, Created)

05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                 Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                      Bahr A., Lauber
Han M., Wiemann
Submitted (JAN-2
                                                                                                                                                                                                                                               TISSUE=Esophagus tumor;
The German cDNA Consortium;
Bahr A., Lauber J., Mewes H
Han M., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; 1
                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Peripheral New Strausberg R.; Submitted (JAN-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182
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P01861; 1ADQ.
Pro. The EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDDEVKFNWYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
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ipheral Nervous
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473 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                       H.W., Weil B.,
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Pred. No. 1.9e
0; Mismatches
                                                                                                                                                                                           EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                    Osanger
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                                                                                                                                                                                                                                                                          Fobo
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S

DKTHTCPPCPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVD

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RESULT 15
Q6N094 HUMAN
ID Q6N094;
AC Q6N094;
DT 05-JUL-2
DT 15SUE=E
RG T1SUE=E
RG T1SUE-E
RG T1SUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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Query Match
Best Local S
Matches 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                      InterPro; IPR00359; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_w.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; C1-set; 3.
SMART; SM00409; IG; 2.
SMART; SM00409; IG; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS00835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 480 AA; 52612 MW; 225247F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF07654; C1-set; 3.

SMART; SM00409; I; 2.

SMART; SM00406; IGC1; 3.

SMART; SM00406; IGV; 1.

SMORT; SM00406; IGV; 1.

PROSITE; PS00835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; UNKNOWN_2

Hypothetical protein.

SEQUENCE 475 AA; 52043 MW; B7EA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGN094_HUMAN PRELIMINARY; PRT; 480 AA. Q6N094; Q6N094; Q6N094; Q6N094; Q6N094; Q7 Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation updat Hypothetical protein DKFZp686001196. Name=DKFZp686001196;
                                                                                                                                                                                                                                                                                                                                                                                          Fobo G., Han M., Wiemann S.; Submitted (JAN-2005) to the EMBL; BX640622; CAE45776.1; HSSP; P01861; 1ADQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Esophagus tumor;
The German cDNA Consortium;
Wambutt R., Heubner D., Mewes H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25
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93.8	93.8	93.8	93.8	93.8	94.1	94.2	94.2		94.2	94.2	94.2			94.2		94.2	94.2	94.3		94.3
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Adc98608	Adm97493	Adx83727	Adm97513	Adx83744	Abp70842	Ado40298	Adf45364	Adg76141	Ado40296	Adf45362	Adg76139	Adc98600	Adc98614	Adc98604	Adc98606	Adc98618	Adc98612	Adc98568	Adc98602	Adc98610
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ALIGNMENTS

RESULT 1 AAB16958 Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; ILI-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; vascular endothelial growth factor; matrix metalloproteinase; 04-MAY-2000. WO200024782-A2 Synthetic. Homo sapiens. thrombosis; pharmaceutical. Fc-TMP protein sequence SEQ ID NO:6. 31-OCT-2000 AAB16958; AAB16958 standard; protein; 247 AA. (first entry)

25-OCT-1999;

99WO-US025044

23-OCT-1998; 22-OCT-1999; 98US-0105371P 99US-00428082

(AMGE-) AMGEN INC.

Feige ۲, Liu C, Cheetham ۲ Boone iO.

WPI; 2000-350702/30. N-PSDB; AAA69444.

Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.

Claim 21; Page 179-180; 608pp; English.

The present invention describes composition of matter (I) comprising (FC domain, pharmacologically active peptides, and linkers. Where (I) (X1)a-F1-(X2)b, where: F1 = an FC domain, X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P 2 , or -(L1)c-P1-(L2)d-P2-(L3)e-P 3 , or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, Ρ2

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RRESULT 2
ABB73411
ID ABB8
XX ABB
XX ABB
XX O5--
DT O5--
XX Mod
XW MMP
XW TNF
XW TNF
XW TNF
XW Cytt
XW Cytt
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Matches 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor; TNF-alpha inhibitor; interleukin I antagonist; II-1 antagonist; TMP; TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antirheumatic; antiarthritic; antidabetic; ophthalmological; cytostatic; antorectic; antiinfertility; antidabetic; dermatological; neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; anaemia; sleep disorder; neurological degenerative disease; anaemia;
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                                      02-MAY-2001; 2001WO-US014310
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Synthetic.
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Pred. No. 4.9e-94;
); Mismatches 0;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cc neuroprotective activities. (I) can be used as a therapeutic or cc prophylactic agent as well as for screening purposes, (I) is useful for cc diagnosting diseases characterised by dysfunction of their associated cc protein of interest, for identifying normal or abnormal proteins of cc interest, as a part of diagnostic kit to detect the presence of their cc proteins of interest in a biological sample. Additionally, (I) is useful for treating inflammatory and autoimmune diseases, tumour growth, cancer, cr rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders, cc infertility, and neurological degenerative diseases. (I), comprising EPO-cc minetic compounds are useful for treating disorders characterised by low cred blood cell levels such as anaemia. The TPO-mimetic comprising compounds are useful for treating disorders characterised by low cred blood cell levels such as anaemia. The TPO-mimetic comprising compounds are useful for treating disorders characterised by low cred blood cell tevels such as anaemia. The TPO-mimetic comprising compounds are useful for treating disorders characterised by low cred blood cell tevels such as anaemia. The TPO-mimetic comprising compounds are useful for treating disorders characterised by low cred blood cell tevels such as anaemia, aplastic anaemia, metastatic cumour which result in thrombocytopaenia, aplastic anaemia, metastatic cumour which result in thrombocytopaenia, aplastic anaemia, metastatic comprises that involve an expected megakaryocyte/platelet efficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet compounds are useful compounds and anaemia 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a vehicle-peptide molecule (I) or its multimers. (I) can have antiinflammatory, antitumour, immunosuppressive, cytostatic, antiheumatic, antiantrinitic, antidabetic, ophthalmological antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
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ilarity 100.0%;
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Pred. No. 4.9e-94;
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Low Low

FC-TMP-TMP

protein sequence SEQ ID NO:8.

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The present invention describes composition of matter (I) comprising an CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (CC (X1)a-F1-(X2)b, F2-(X1)c-F1-(X1)c-F1-(X2)d-F2-(X1)c-F2-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c-F1-(X1)c
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22-OCT-1999;
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cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
vascular endothelial growth factor; matrix metalloproteinase; asthma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          composition of matter comprising an Fc domain and pharmacologically e peptides, useful for treating cancer and autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGGIEGPTLR
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Pred. No. 5.4e-94;
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neuroprotective activities. (I) can be used as a therapeutic or compounds are useful for red blood cell levels such as anaemia. The TPO-mimetic compounds are useful for red blood cell levels such as anaemia, seystemic, saystemic, such as anaemia, such as anaemia, such as a part of diagnostic kit to detect the presence of their proteins of interest in a biological sample. Additionally, (I) is useful for treating inflammatory and autoimmune diseases, tumour growth, cancer, infertility, and neurological degenerative diseases. (I), comprising EPO-mimetic compounds are useful for treating disorders characterised by low red blood cell levels such as anaemia. The TPO-mimetic compounds are useful for treating disorders characterised by low megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency as thrombocytopaenia, aplastic anaemia, metastatic cumour which result in thrombocytopaenia, systemic lupus erythematosus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; lerythropoietin; TPO; tumour necrosis factor alpha inhibitor; TWF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP; TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antirceumatic; antiinfertiiit; antidabetic; ophthalmologic antianaemic; anorectic; antiinfertiiity; haemostatic; dermatological; neuroprotective; inflammatory disease; autoimmune disease; tumour grow cancer; rheumatoid arthritis; diabetic retinopathy; infertiity; obes; sleep disorder; neurological degenerative disease; anaemia; thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a vehicle-peptide molecule (I) or its multimers. (I) can have antiinflammatory, antitumour, immunosuppressive, cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 8; 176pp; English
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exemplification
A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP] 1-(L 1) nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 14 residues in length comprising x_2-X_1_0, x_2-X_1_1, x_2-X_1_2, x_2-X_1_3, x_2-X_1_4, x_1-X_1_0, x_1-X_1_1, x_1-X_1_2, x_1-X_1_2, x_1-X_1_3, and x_1-X_1_3, x_2-X_1_4, x_1-X_1_0, x_1-X_1_1, x_1-X_1_2, x_1-X_1_2, x_1-X_1_3, and x_1-X_1_3, x_1-X_1_3, a
                                                                                                                                                                                                                                                                              Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment diseases which involve thombocytopenia.
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N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Modified peptide; therapeutic agent; fusion; Pc domain; cancer autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VI immunosuppressive; EPO; TPO; CTLA4; mimetic; II-1; TNF; antago; inhibitor; erythropoietin; thrombopoietin; interleukin ; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; thrombosis; pharmaceutical.
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22-OCT-1999;
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Local Similarity 100.0%; Pred. No. 5.9
hes 247; Conservative 0; Mismatches
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                erythropoietin; TPO; tumour necrosis factor alpha inhibitor; TMP; TMP-alpha inhibitor; interleukin 1 antagonist; TMP; TMP-alpha inhibitor; interleukin 1 antagonist; TMP; TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; Cyrostatic; antiinflammatory; antiinfumour; immunosuppressive; Cyrostatic; antirheumatic; antiarthritic; antidabetic; ophthalmological; antianaemic; anorectic; antiinfertility; haemostatic; dermatological; neuroprotective; inflammatory disease; autoimmune disease; tumour grov cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obes: sleep disorder; neurological degenerative disease; anaemia; thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                             05-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                          ABB73423 standard;
                                                                                                                                                                                                                                                                      Fc-VEGF antagonist fusion nucleic acid SEQ ID
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tumour necrosis factor alpha inhibitor;
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99.6%;
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Pred. No. 4.5e-89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exemplification of the present invention
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RESULT 8 AAB17953 ID AAB1

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                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes composition of matter (I) comprising an CC Pc domain, pharmacologically active peptides, and linkers. Where (I) is: CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each cc independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L2)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, CC (L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, CC (L2)d-P3-(L3)e-P3-(L4)f-P4 where P1, P2, CC (L2)d-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)f-P4-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P3-(L4)e-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; autoimmune disease; cytostatic; anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fc-IL-1 antagonist fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17953;
                                                                                                                                                                                                                                                                                                                                                             Sequence
                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              composition of matter comprising e peptides, useful for treating ca
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                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Page 574-575; 608pp;
KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWBSNGQPENNYKTTPPVLD
                                                                                                            DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKBYKCKVSNKALPAPIEKTISKA
                                                                                                                                                                                                                   MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                                            DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                                                       MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C,
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry
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99US-00428082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheetham
                                                                                                                                                                                                                                                                                        94.9%;
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                                                                                                                                                                                                                                                               Score 1273; DB 3;
Pred. No. 7.5e-89;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ng an Fc domain and pharmacologically cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fusion;
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                                                                                                                                                                                                                                                                                                              Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antagonist; MMP;
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cc neuroprotective activities. (I) can be used as a therapeutic or cc prophylactic agent as well as for screening purposes. (I) is useful for cc diagnosing diseases characterised by dysfunction of their associated cc protein of interest, for identifying normal or abnormal proteins of cc interest, as a part of diagnostic kit to detect the presence of their cc proteins of interest in a biological sample. Additionally, (I) is useful cf for treating inflammatory and autoimmune diseases, tumour growth, cancer, cc infertility, and neurological degenerative diseases. (I), comprising EPO-cc mimetic compounds are useful for treating disorders characterised by low red blood cell levels such as anaemia. The TPO-mimetic comprising cc empathence are useful for treating disorders characterised by low red blood ser useful for treating conditions that involve an existing compounds are useful for treating conditions that involve an existing compounds are useful for treating conditions that involve an existing compounds are useful for treating conditions that involve an existing compounds are useful for treating conditions that involve an existing compounds are useful for treating disorders anaemia, metastatic deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic tumour which result in thrombocytopaenia, systemic lupus erythematosus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; antianaemic; ancrectic; antiinfertility; haemostatic; dermatological; neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; anaemia; sleep disorder; neurological degenerative disease; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TPO mimetic peptide; EPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a vehicle-peptide molecule (I) or its multimers. (I) can have antiinflammatory, antitumour, immunosuppressive, cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAY-2000; 2000US-00563286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified peptide;
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DB; ABL35771.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C,
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The specification describes a method of decreasing the incidence of an immune reaction in a subject who is given a therapeutic composition comprising a (potentially) immunogenic therapeutic molecule, tolerizing a subject to such a molecule, or decreasing the antibody titer in a subject administered such a molecule. The method comprises administering CTLA-4 to the subject within an effective time interval relative to the administration of the therapeutic composition. The CTLA-4 may further comprise an immunoglobulin heavy chain constant region. The method of the invention is useful for modulating an immune response to an immunogenic therapeutic agent. The present sequence represents a mL63-9 peptide fused
                                                                                                                                                                                                                                                                                                                                                                                        Decreasing immune reactions in a subject treated with a (potentially) immunogenic therapeutic molecule comprises administering CTLA-4 within effective time interval relative to the administration of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  viper;
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Composition comprising integrin or adhesion antagonistic vehicle, useful for treating or preventing platelet aggre longer half-life than free peptide.

istic peptide aggregation,

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Feige

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Kohno T,

Lacey DL,

Boone

TC;

2002-062025/08 DB; ABK24109.

Example 1; Page 45-46; 68pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 236;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADN59746 standard; protein;
                                                                                                                                                                                                                 thrombocytopaenia; aplastic anaemia; autoimmune autoimmune haemolytic anaemia; Hughe's syndrome
                                                                                                                                                                                                                                                                                transmembrane signaling; mpl receptor; thrombopoietin m TMP; c-mpl receptor; platelet precursor; megakaryocyte;
                                                                                                                                                                                                                                                                                                                                                 Haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                               Vector 20003182 encoded amino acid sequence, seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-2004
17-APR-2003
                                                              WO2003031589-A2
                                                                                                                            Unidentified
                                                                                                                                                                                       lupoid thrombocytopaenia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
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                                                                                                                                                                                                                                                                                                                                                 antianaemic; immunosuppressive; platelet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.7%;
97.5%;
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Pred. No. 1.5e-88;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                    thrombopoietin mimetic peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 282;
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RESULT 13
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The invention relates to a thrombopoletin mimetic peptide (TMP) (I) that combined to the c-mpl (mpl) receptor, and which stimulates the production of platelet precursors, is new Further cdisclosed is a composition of matter (II) that binds to an mpl receptor, and a pharmaceutical composition of matter (II) that binds to an mpl receptor, and a pharmaceutical composition of the invention is useful for treating thrombocytopaenia in an animal, and for increasing megakaryocytes or conditions involving a megakaryocyte and/or platelet deficiency, e.g. conditions involving a megakaryocyte and/or platelet deficiency, e.g. conditions involving thrombocytopaenia such as aplatelic anaemia, autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia, canaemia, hughe's syndrome and lupoid thrombocytopaenia. The TMP of the invention is also useful for megakaryocytes and its derived cells. The compounds demonstrate an improved ability to bind to and/or trigger transmembrane signal through, i.e. activating, the mpl receptor the compounds have superior thrombopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity and in vivo circulation time. The current sequence represents the amino acid sequence encoded by a vector for use in constructing C-terminal Fc fusion compounds (i.e. peptide attached at its constructing C-terminus of the Fc).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2002; 2002WO-US032552
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                                                                                                                                                                                                                                                               MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPBVTCVVVDVSHEDPEVKFNWYV
                                                                                                                KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
                                                                                                                                                                                DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                    SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSFGKGGGGGIE
                                                                                                                                                                                                                                          MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
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                                                                            KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
                                                                                                                                                           DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001US-0328666P.
2002US-00269806.
                                                                                                                                                                                                                                                                                                                                                                                                    A
A
                                                                                                                                                                                                                                                                                                                                                                                                                                            C-terminus
                                                                                                                                                                                                                                                                                                                                          94.6%;
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                                                                                                                                                                                                                                                                                                                     Score 1269; DB 7;
Pred. No. 1.5e-88;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                            of the
                                                                                                                                                                                                                                                                                                                                                                                                                                              FC)
                                                                                                                                                                                                                                                                                                                                                               DB 7;
                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                  CC The present invention describes composition of matter (I) comprising an CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is: CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each CC independently selected from -(L1)c-F1, -(L1)c-F1-(L2)d-F2, -(L1)c-F1-(L2)d-F2, -(L1)c-F1-(L2)d-F2, -(L1)c-F1-(L2)d-F2-(L3)e-F3, or -(L1)c-F1-(L2)d-F2-(L3)e-F3-(L4)f-F4 where F1, F2, CC (L2)d-F2-(L3)e-F3, or -(L1)c-F1-(L2)d-F2-(L3)e-F3-(L4)f-F4 where F1, F2, CC (L2)d-F2-(L3)e-F3-(L4)f-F4 where F1, F2, CC (L2)d-F2-(L3)e-F3-(L2)f-F2-(L3)e-F3-(L4)f-F4 where F1, F2, CC (L2)d-F2-(L3)e-F3-(L2)f-F2-(L3)e-F3-(L4)f-F4 where F1, F2, CC (L2)d-F2-(L3)e-F3-(L2)f-F2-(L3)e-F3-(L4)f-F4 where F1, F2, CC (L2)d-F2-(L3)e-F3-(L3)f-F3-(L2)f-F4-(L2)d-F2-(L3)e-F3-(L4)f-F4-(L2)d-F2-(L3)e-F3-(L4)f-F4-(L2)d-F2-(L3)e-F3-(L4)f-F4-(L2)d-F2-(L3)e-F3-(L4)f-F4-(L2)d-F2-(L3)e-F3-(L4)f-F4-(L2)d-F2-(L3)e-F3-(L4)f-F4-(L2)d-F2-(L3)e-F3-(L4)f-F4-(L2)d-F2-(L3)e-F3-(L4)f-F4-(L2)d-F2-(L3)e-F3-(L4)f-F4-(L2)d-F2-(L3)e-F3-(L4)f-F4-(L2)d-F2-(L3)e-F3-(L3)f-F4-(L2)d-F2-(L3)e-F3-(L3)f-F3-(L3)f-F3-(L3)f-F
                                                                                                                                                                                                                                                                   Query Match
Best Local Sin
Matches 233;
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feige
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-1998;
22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fc-MMP inhibitor fusion protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                             Local Similarity
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121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         composition of matter comprising an Fc domain and pharmacologically peptides, useful for treating cancer and autoimmune diseases.
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                                                                                                             DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                                                                                     MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
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                            KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
                                                                                                                                                                             MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                   94.68;
                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                   Score 1268; DB 3;
Pred. No. 1.8e-88;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                              Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer;
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neuroprotective activities. (I) can be used as a therapeutic or prophylactic agent as well as for screening purposes. (I) is useful for diagnosing diseases characterised by dysfunction of their associated protein of interest, for identifying normal or abnormal proteins of interest in a biological sample. Additionally, (I) is useful for treating inflammatory and autoimmune diseases, tumour growth, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders, infertility, and neurological degenerative diseases. (I), comprising EPO-mimetic compounds are useful for treating disorders characterised by low red blood cell levels such as anaemia. The TPO-mimetic comprising compounds are useful for treating conditions that involve an existing megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet cumour which result in thrombocytopaenia, systemic lupus crythematosus, and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a wehicle-peptide molecule (I) or its multimers. (I) can have antiinflammatory, antitumour, immunosuppressive, cytostatic, antitheumatic, antiarthritic, antidabetic, ophthalmological antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; erythropoietin; TPO; tumour necrosis factor alpha inhibitor; TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP; TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antirheumatic; antiafarthitic; antidiabetic; ophthalmologiantianaemic; anorettic; antiinfertility; hemotatic; dermatological; neuroprotective, inflammatory disease; autoimmune disease; tumour graceancer; rheumatoid arthritis; diabetic retinopathy; infertility; obes sleep disorder; neurological degenerative disease; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7; Fig 25A-B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-2000; 2000US-00563286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C,
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Best Local S
Matches 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17951
The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (XI)a-F1-(XZ)b, where: F1 = an Fc domain; X1 and X2 are independently selected from -(L1)c-P1-(L2)d-P2-(L3)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active
                                                                                                                                                                                                                                   Novel composition of active peptides, usef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                     Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; protein; 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
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                                                                                                                                                                                     568-569; 608pp; English
                                                                                                                                                                                                                                         n of matter
useful for
                                                                                                                                                                                                                                                                                                                                                                                                   Cheetham
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100.0%;
                                                                                                                                                                                                                                   ster comprising an Fc domain and pharmacologically for treating cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1268; DB 5;
Pred. No. 1.8e-88;
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 248
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                     SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGG
                                                                                                   KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
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                                                                                                                                                                                                                                                                       MDKTHTCPPCDAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYV
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                                                                                                                                                                                      DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
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SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHBALHNHYTQKSLSLSPGKGGGGG
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C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interactions of cloned gene produc A;Reference number: S31886
A;Accession: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 FIL>
A;Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:g33068; PIDN:CAA49866.1;
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region
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RESULT 2 GHHU Ig gamma C.Specie C.Date: C.Access R.Elliso Nucleic A;Title: A;Refere A;Access A;Molecu	9d 4d) b	Q	Db	γŞ	υь	Q	Que: Best Mati
RESULT 2 GGHHU Ig gamma-1 chain C region - human C;Species: Homo sapiens (man) C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004 C;Accession: A9343; S36861; S33887; B90563; A90564; B91668; A91723; A02146 R;Ellison, J.W.; Berson, B.J.; Hood, L.E. Nucleic Acids Res. 10, 4071-4079, 1982 A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene. A;Reference number: A93433; MUID:82274238; PMID:6287432 A;Molecule type: DNA	209 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 255	GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP	122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181	89 GVEVHNAKTKPREBQYNSTYRVVSVLTVLHQDWLNGKBYKCKVSNKALPAPIEKTISKAK 148	62 GVEVHNAKTKPREEQYNSTYRVVSYLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121	29 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 88	2 DKTHTCPPCPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 61	Query Match 91.9%; Score 1233; DB 4; Length 255; Best Local Similarity 100.0%; Pred. No. 8.6e-88; Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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A;Molecule type: protein

A;Molecule type: protein

A;Residues: 1-96, R', 98-197, D', 199-238, 'E', 240, 'M', 242-266, 'D', 268

A;Cross-references: UNIPARC:UPI0000173790

A;Note: this sequence has the Glm(3) and Glm(non-1) markers

R;Gall, W.E.; Edelman, G.M.

Biochemistry 9, 3188-3196, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. X

A;Reference number: A90565; MUID:71064027; PMID:4923144

A;Contents: annotation; disulfide bonds

R;Dreker; L.; Schwarz, J.; Reichel, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976

A;Title: Rule of antibody structure. The primary structure of monocal enbromide cleavage products, and the disulfide bridges.

A;Reference number: A91667; MUID:77070267; PMID:1002129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 1-96, 'R', '98-135 < CUN'
A; Residues: 1-96, 'R', '98-135 < CUN'
A; Cross-references: UNIPARC: UPI000017378D
A; Note: this sequence has the Glm(3) marker, 'S
R; Ruttishauser, 'U'; Cunningham, B.A.; Bennett,
B; Cochemistry 9, 3171-3181, 1970
A; Title: The covalent structure of a human gan
A; Reference number: A90564; MUID:71064025; PMI
A; Reference number: A90564; MUID:71064025; PMI
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A;Cross-references: UNIPROT:P01857; UNIPARC:L
A;Note: this sequence has the Glm(17) alloty;
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: this sequence has the Glm(non-1) markers, 239-Glu R;Ponstingl, H.; Hilschmann, N. Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976 A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: UNIPARC:UPI000017378B; R;Cunningham, B.A.; Rutishauser, U.; Gall, Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human A;Reference number: A90563; MUID:71064024; A;Contents: myeloma protein Eu A;Accession: B90563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPARC:UPI000013C6FE; EMBJ
R;Takahashi, N; Ueda, S.; Obata, M.; Nikaido,
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamm
A;Reference number: S33887; MUID:83001943; PMII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data A; Reference number: $33904
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: this sequence has the Glm(17) and Glm(1) markers R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N. Hoppe-Seyler's Z. Physiol. Cham. 364, 713-747, 193 A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen A;Reference number: A91723; MUID:83289131; PMID:6884994 A;Contents: myeloma protein KOL; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: A91668;
A;Contents: myeloma protein
A;Accession: B91668
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A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E'
A;Cross-references: UNIPARC:UPI000017378E
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A; Contents: annotation; C; Genetics:
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A;Residues: 88-113;235-330
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A;Accession: A91723
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A;Cross-references: UNIPARC:UPI000017378F
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;Residues: 2-330 <HAR>
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Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1)
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PMID:6811139
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PMID:4923144
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pMID:5530842
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PMID:5489771
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, C.; Konigsberg, W.H.; Bdelman,
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kanaling the constant) in some cases, such as IgA and IgW, the subunits associate into 1 C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-85/Domain; immunoglobulin homology <IM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;243-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: UNIPARC:UP10000176F25; EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eur. J. Blochem. 229, 54-60, 1995

A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition A;Reference number: 869339; MUID:95262687; PMID:7744049

A;Accession: 869339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S63339; S72664
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A; Introns: 99/1; 114/1; 224/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: S72664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data
A; Reference number: S72664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Khamlichi, A.A.; Aucouturier,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Khamlichi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-374 < KHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
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208
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                                    GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
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GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                      DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
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99.1%;
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; Pred. No. 1.2e-87;
0: Mismatches 0;
                                                                                                                                                                                                               Score 1227; DB 2;
Pred. No. 4e-87;
2; Mismatches 0;
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R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc
A;Reference number: PT0207; MUID:91287716; PM
A;Accession: PT0207
A;Molecule type: mRUA
A;Residues: 1-234 <EHR>
A;Residues: 1-234 <EHR>
C;Superfamily: immunoglobulin C region; immun
C;Keywords: immunoglobulin homology <IMM
F;48-117/Domain: immunoglobulin homology <IMM
                                               Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region A;Ritle: Sequence of a human immunoglobulin gamma 3 heavy chain constant region A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Recession: A23511
A;Recession: A23511
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:g33070; PID C;Genetics:
A;Genetics: A;Genecics: GDB:GHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Interons: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                       A23511
If gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
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R;Ehrlich, P.H.; Moustafa, Z.A.; Oestbe
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Best Local Similarity
Matches 217; Conserv
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  85.5%;
92.5%;
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Pred. No. 9.3e-84;
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1146; DB 2;
No. 7.1e-81;
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PMID:2062315
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Ig gamma-3 chain C re
C;Species: Homo sapie
C;Date: 14-May-1993 #
C;Accession: A60764
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Apace: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma hea A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Ecsidues: 1-326 <ELL>
A;Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Acresion: A60764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-377 <HUC>
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:QBN4Y9; UNIPARC:UPI0000176F0B
C;Superfamily: immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
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Best Local S
Matches 210
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Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQPREPQVYTLPPGREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS
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92.5%;
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Pred. No. 1e-80;
8; Mismatches
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GB:V00554; GB:J00230; NID:g

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A;Note: Lys-326 is probably removed posttranslationally R;Wang, A.C.; Tung, B.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q', 21-57,'Z',59,'A',61-193,'D',195-325 <WANA;Cross-references: UNIPARC:UPI0000173791
A;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Blochem. 57, 758-767, 1979
Can. J. Blochem. 57, 758-767, 1979
Can. J. Blochem. 57, 758-767, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human : A;Reference number: A90253, MUJD:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bor R;Prangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUJD:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: GDB:IGHG2

A;Cross-references: GDB:119338; OMIM:147110

A;Cross-references: GDB:119338; OMIM:147110

A;Map position: 14q32.33-14q32.33

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F;20-85/Domain: immunoglobulin homology <IMI>
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A;Residues: 238-275 <ABOP>
A;Crose-references: UNIPARC:UPI0000173794
A;Confenn, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: A note on the amino acid sequence A;Reference number: A93132; MUID:80114419; A;Contents: Zie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
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A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198
A;Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793
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Best Local (
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                                                                                                               106
165
                                                      67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.; Frangione,
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                                                                                                               CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                                                                                                                                                                                                                                                                                                                                    site: carbohydrate (Asn)
                                       NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
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94.1%;
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; PMID:6774012
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      RESULT
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F;99-110/Region: "Have F;99-110/Region: "Immunoglobulin homology <IM2>
F;134-203/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;14/Disulfide bonds: interchain (to heavy chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: heavy chain) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 1432.33-1432:33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin c region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin p;20-65/Domain: immunoglobulin homology <IM1>
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A; Residues: 1-327 < ELL>
A; Residues: 1-327 < ELL>
A; Cross-references: UNIPROT: P01861; UNIPARC: UPI0000047190
A; Note: the sequence was determined from the germline gene
R; Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A; Title: Human immunoglobulin sublclasses. Partial amino ac
A; Reference number: A90249; MUID: 70207560; PMID: 4192699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision
C;Accession: A90933; A90249; A02150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;KeSIQUES: 1-30;81-326 <PIN>
A;Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Nucleotide sequence of a human immunoglobulin of A; Reference number: A90933; MUID:83157104; PMID:6299662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Ellison, J.; Bux
DNA 1, 11-18, 1981
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A;Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A90249
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                                                                                                                                                                                              166 NAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPRE
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                                   LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
                                                                                                                                                                                                                        NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
                                                                                                                                                                                                                                                                                               CPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH
                                                                                                                                                                                                                                                                                                                           CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
                                                                                                                            PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
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93.7%;
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Pred. No. 4.2e-80;
B; Mismatches 6
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G3HUWI

G3HUWI

G3HUWI

G3HUWI

C; parma-3 heavy chain disease proteins - human

C; parcies: Homo sapiens (man)

C; parcies: Homo sapiens (man)

C; parcies: J1-Dec-1979 #sequence revision 23-Oct-1981 #text_change 16-Jul-1999

R; parcies: J1-Dec-1979 #sequence revision gamma3 immunoglobulin deletion mutant: gamma3 heavy-A; parcies: par
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-157
A;Cross-references: UNIPARC:UPI000017379A; UNIPARC:UPI000017379C;
A;Note: a carboxyl-terminal Lys is removed posttranslationally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: gamma heavy chain disease in man: cDNA sequence supports A;Reference number: A93915; MUID:82247835; PMID:6808505 A;Contents: heavy chain disease protein Omm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: Cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C. Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein A;Reference number: A99198; MUID:77021516; PMID:823945
A;Contents: heavy chain disease protein Zuc, partial sequence corr A;Accession: A90198
A;Accession: A90198
A;Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
A;Cros-references: UNIPARC:UPI0000173799
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C; Superfamily: i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: this protein lacks most of the V region, all of the R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, I Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: A92219
A;Molecule type: protein
A;Residues: 12-97 <MIC>
A;Cross-references: UNIPARC:UPI0000173798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Primary structure of the 'hinge' region of human A;Reference number: A92219; MUID:77118561; PMID:402363 A;Contents: normal gamma-3 chains, sequence corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note: the hinge region in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      idue segment (12-28)
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                superfamily: immunoglobulin C region; immunoglobulin homology keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid; 203-270/Domain: immunoglobulin homology <IMM>; I/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental; I/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                       ;6,140/Binding site: carbohydrate (Asn)
                                                                                                                                64
                                                                                                                                                                                                                                                                                                       Similarity
                                                        GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
                                                                                                                                                                   DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                            DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVD
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Pred. No. 4
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В.; 1
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91

MDKT---HTC--PPCPAPELL/GGPSVELFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVK 55

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A;Reference number: A917-A;Accession: A91749
A;Accession: A91749
A;Molecule type: mRNA
A;Residues: 1-323 <BER>
A;Cross-references: UNIPI
                                                                                                                                                                                                            C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kindain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into ] C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-82/Domain: immunoglobulin homology <IM1> F;130-199/Domain: immunoglobulin homology <IM2> F;236-303/Domain: immunoglobulin homology <IM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.

Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982

A;Title: Heavy chain genes of rabbit IGG; isolation of a cDNA encoding gamma heavy c A;Reference number: A93928; MUID:83299917; PMID:6193512

A;Accession: A93928

A;Accession: A93928; MUID:83299917; PMID:6193512

A;Accession: A93928

A;Coss-references: UNIPARC:UPI000016C5ED; GB:M16426; NID:9165111; PIDN:AAA31289.1; A;Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic m, Note: this sequence has the d11 allotypic marker, R.R.

Biochem. J. 116, 249-259, 1970

A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobu A;Peference number: A90245; MUID:70110015; PMID:5461106
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R;Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A;Title: Sequence studies on the constant re;
A;Reference number: A90290; MUID:76135469; P]
A;Accession: A90290
A;Molecule type: protein
A;Residues: 1-47, E', 49-71, PV', 72-128 < PRA>
A;Residues: 1-47, E', 49-71, PV', 72-128 < PRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 132-143, 'E', 145-161 <FRU>
A;Cross-references: Unitable Colonial Colonial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E'
A;Cross-references: UNIPARC:UPI00001737AD; UNIPARC:UPI00001737AE
A;Note: this has the e15 allotypic marker, 185-Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 24-Apr-1984 #sequence revision 15-Nov-1984 #t
C;Accession: A91749; A90290; A93928; A90245; A94416;
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
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GHRB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                            ;173/Binding site: carbohydrate (Asn)
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                                                 Pred.
                                                                                      Score
         Mismatches
                                                 918.5;
No. 2e-
                                                                                                                                                                                (covalent)
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                                                                                      ВВ
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6; A02161
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Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #te
C;Accession: 147159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identif
A;Reference number: 147158; MUID:95015845; PMID:793057
A;Recession: 147159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC-
A;Cross-references: UNIPARC:UPI0000115524; EMBL:U03779
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulir
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C.Species: Sus scrota domestica (domestic pig)
C.Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #t
C.Accession: 147160
R; Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A, Title: Five putative subclasses of swine IgG identi
A; Reference number: 147158; MUID:95015845; PMID:79305
A, Accession: 147160
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: mRNA
A, Residues: 1-328 KAC-
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C;Superfamily: imn
F;133-202/Domain:
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Best Local S
Matches 164
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73.2%;
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Pred. No. 1.7e-62;
9; Mismatches 28;
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            immunoglobulin homology
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                                                                       EMBL: U03779;
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                                                                     NID: g433123;
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                                                                         PIDN: AAA52217.1;
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                                                                           PI
A;Reference number: A94553
                              Ig gamma-2 chain C region - guinea pig C;Species: Cavia porcellus (guinea pig) C;Date: 07-May-1981 #sequence_revision C;Accession: A94553; A90352; A90359; A9 R;Trischmann, T.M. submitted to the Atlas, April 1975
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RESULT

14

A90384;

07-May-1981 #text_change 09-Jul-2004 90384; A90385; A02151

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R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine
A;Reference number: 147158; MUID:95015845;
A;Accession: 147162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
147162
19 gamma 4 chain constant region - pig (fragment)
19 gamma 4 chain constant region - pig (fragment)
19 gamma 4 chain constant region - pig (fragment)
19 Species: Sus scrofa domestica (domestic pig)
10 C;Species: 21-Feb-1997 #sequence_revision 21-Feb-1997
10 C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997
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C;Superfamily: ir
F;82-151/Domain:
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A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
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                                                                                                                                                                                                                                                                                                                                ;Superfamily: immunoglobulin C
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                                                            165 TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164;
 223
                              174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPICPACE-SPGPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPBVTCVVVDVSHEDPEVKFNMYVDGVEVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POVYTLPPHAEELSRSKVSITCLVIGFYPPDIDVEWORNGOPEPEGNYRTTPPOODVDGT
                   TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                          FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK
                                                                                                                                                                                         VDKRVGTKTKPPCPICPACEGPGPSAFIFPPKPKDTLMISRTPKVTCVVVDVSQENPEVQ
TTPPQQDVDGTYFLYSKLAVDKASWQRGDTFQCAVMHEALHNHYTQKSIFKTPGK
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                                                                                                                                                                                                                                                                                                              immunoglobulin
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                                                                                                                                                                                                                                                    67.4%; Score 903.5; DB 2
71.1%; Pred. No. 2.3e-62;
tive 30; Mismatches 31
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                                                                                                                                                                                                                                                                                                                region; immunoglobulin
homology <IMM>
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Pred. No. 1.7e-62;
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C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;21-81/Domain: immunoglobulin homology <IM1>
F;135-204/Domain: immunoglobulin homology <IM2>
F;241-310/Domain: immunoglobulin homology <IM3>
F;28-79/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blochemistry 10, 26-31, 1971

A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.

A;Reference number: A90354; MUID:71058474; PMID:4922544

A;Rontents: annotation; disulfide bonds

A;Note: Cys-16 is involved in a heavy-light chain bond

A;Note: Cys-16; Cys-107, Cys-107, and Cys-110 form inter-heavy chain bonds

C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c);Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c);Complex: An immunoglobulin heterotetramer subunit of two identical light (kap c);Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c);Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c);Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c);Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c);Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c);Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c);Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c);Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c);Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c);Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c);Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c);Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c);Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c);Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c);Complex: An immunoglobulin light (kap c);Complex: An immunoglobulin light (kap c);Complex: An immun
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Biochemistry 10, 9-17, 1971
Biochemistry 10, 9-17, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2).
A;Reference number: A90359; MUID:71058486; PMID:5538616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A94553
A;Molecule type: protein
A;Residues: 1-3 <TRI>
A;Cross-references: UNIPROT:P01862; UNIPARC:UPI000017379E
A;Cross-references: UNIPROT:P01862; UNIPARC:UPI000017379E
B;Chemistry 10, 18-25, 1971
Biochemistry 10, 18-25, 1971
A;Title: Structure of heavy chain from strain 13 guinea pi
A;Reference number: A90352; MUID:71058471; PMID:5538606
A;Accession: A90352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A;Reference number: A90385, MUID:75036073; PMID:4609467
A;Accession: A90385
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A;Title: Primary structure of the C-H2 homology region
A;Reference number: A90384; MUID:75036072; PMID:4429665
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A;Residues: 69-133;312-329 <TUR>
A;Cross-references: UNIPARC:UPI00001737A0; UNIPARC:UPI00001737A1
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A; Residues: 227-311 <TR2>
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Best Local S
Matches 162
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    184
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                                                                                                                                                                                                                                                                                                       HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNXALPAPIEKTISKAKGQPR 125
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                   EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDG
                                                                                                                                                                                                                                                          GNAETKPRVEQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                  TCPKCPPPENLGGPSVFIFPPKPKDTLMISLTPRVTCVVVDVSQDEPEVQFTWFVDNKPV 165
                                                                                 MPDVYTLPPSRDELSKSKVSVTCLIINFFPADIHVEWASNRVPVSEKEYKNTPPIEDADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 889; DB 1;
Pred. No. 3.8e-61;
4; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 329
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R;Kacskovics, I:; Sun, J:; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified A,Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47158
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
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C;Superfamily: immunoglobulin C region; immunog
F;133-202/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
I47158
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PDB; ID6X; X-ray; H=1-102.

PDB; IFC1; X-ray; A/B=106-339.

PDB; IFC2; X-ray; A/B=106-329.

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PDB; II7Z; X-ray; H/K=1-330.

PDB; II17Z; X-ray; H/K=1-330.

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RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butkesley R.W., Touchman J.W., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                             Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC073766; AAH73766.1; -; mRNA.

R GO; GO:0016021; C:integral to membrane; IEA.

InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003597; Ig c1.

R InterPro; IPR003596; Ig w.

R InterPro; IPR003596; Ig v.

R InterPro; IPR003596; Ig v.

R SMART; SM00409; IG; 2.

R SMART; SM00409; IG; 2.

R SMART; SM00407; IGc1; 3.

R SMART; SM00407; IGc1; 3.

R SMART; SM00406; IGv 1.

R PROSITE; PS50835; IG LIKE; 4.

PROSITE; PS50835; IG MHC; UNKNOWN 2.
  PROSITE; PS50
PROSITE; PS00
Hypothetical
SEQUENCE 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein. Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                       Strausberg R.
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Mammalia; Eutheria;
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HUMAN
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                                                                                                                                                                                                                                                                                                                                            B-Cells;
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  51083 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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  B3A9B7D0FDB1386E CRC64;
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RESULT
Q61N78
ID 107
Q61N78
AC Q61N78
GN DT Q6
GN DT Q6
GN N Q6
OC H Q7
OC H Q6
OC H Q
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                                                                                                                                                                                                                                                                                                                                                                                                                        RP NUCLEOTIDE SEQUENCE.

RP TISSUE-Peripheral Nervous System;

RZ TISSUE-Peripheral Nervous System;

REDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE-2388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE-2388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE-2388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE-2388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

RX MILST N. JORGHAM H., Schamer L., Schemer T.E., Shar N. J., Wang J., Hels N. J., Schemer T.E., Scheme
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Best Local Simi
Matches 227;
Submitted (JUN-2004) to the EMBL; BC072419; AAH72419.1; HSSP; P01861; 1ADQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homin
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                  TISSUE=Peripheral Nervous
NIH MGC Project;
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Name=IGHG1;
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                                                                                                                                                                                                                                                                                                                                                                                                     cDNA sequences.";
l. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Last annotation update)
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Pred. No. 4.3e-91;
                                                                                                                                                                                                                                                                                                                                                                                                     99:16899-16903 (2002)
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Best Local S
Matches 227
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SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOI
SEQUENCE 466 AA; 50854 MW;
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Q569F4;
10-MAY-2005 (
TISSUE-Lymph;
NIH MGC Project;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC092518; AAH92518.1; -; mRNA.
SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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Name=IGHG1;
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10-MAY-2005 (TrEMBLrel.
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Best Local Similarity
Matches 227; Conserv
HSSP; PO1857; 1HZH.
HSSP; PO1857; 1HZH.
SMR; Q7Z7P5; 20-469.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_v.
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01-OCT-2003
01-OCT-2003
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Q7Z7P5_1
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                                                                                                                     Submitted (APR-2003) to the EMBL; BC051328; AAH51328.1;
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NIH MGC Projec
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l. Acad. Sci. U.
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Euarchontoglires; Primates; Catarrhini; Hominidae;
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Pred. No. 4.3e-91;
0; Mismatches 0;
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                                                                                                                                                                                                                                                              AKEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
AKIausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
AA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
AA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
AA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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AA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
AA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang L.,
AB Hopkins R.F., Jordan H., Moore T., Max S.I., Wang L.,
AB Hopkins R.F., Jordan H., Moore T., Max S.I., Wang L.,
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AB Hopkins R.F., Jordan H., Jordan R., Carninci P., Prange C.,
AR Hopkins R.F., Jordan R., Toshiyuki S., Carninci P., Prange C.,
AR Hopkins R.F., Jordan R.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
AR Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
AR Hopkins S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
AR Hopkins S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
AR Hopkins S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
AR Hopkins S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
AR Hopkins S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
AR Hopkins S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
AR Hopkins S., Alley M., Sodergren B.J., Lu X., Gibbs R.A.,
AN Hollan B., Touchman M., Madan A., Rodrigues S., Sanchez A.,
AR Hopkins S., Morley K.C., Shevchenko Y., Bouffard G.G.,
AR Hopkins S., Morley K.C., Green B.D., Dickson M.C.,
AR Hopkins R.M., Touchman J.W., Green B.D., Dickson M.C.,
AR Hopkins R.M., Krzywinski M.I., Schalska U., Smailus D.E.,
B., Cherth A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",

"Forc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Best Local S
Matches 227
                                                           EMBL;
                                                                                                             Strausberg R.;
Submitted (JUN-2003)
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Homo sapiens (Human)
Eukaryota; Metazoa; Cl
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                            ; BC053984; AAH53; ; P01857; 1HZH. rPro; IPR007110;
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RESULT 7

Q6PJA4 HMAN

ID Q6PJA4 HA

AC Q6PJA4;

DT 05-JUL-2

R MADLEOTI

RC TISSUB-P

RX MEDLINE-

RA Altschull

RA Altschull

RA Altschull

RA Altschull

RA Altschull

RA Stapletc

RA Richards

RA Stapletc

RA STAR STAR

ROMERST

RA Whiting

RA Blakeg

RA Stapletc

RA Rodrigue

RA Stapletc

RA STAR

ROMERST

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RS Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RS Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Morley K.C., Morley R.M.,
RA Richards S., World S., Worley R.M.,
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InterPro; IPR003596; Ig_V.
Pfam; PP07654; C1-set; 3.
SMART; SM00406; IGV; 1.
SPROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS500290; IG_MHC; UNKNOWN 2.
HYPOTHECICAL PROSITE; Immunoglobulin domain.
HYPOTHECICAL PROSITE; IMMUNOGLOBULIN DOMAIN.
SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A
   NUCLEOTIDE SEQUENCE.
TISSUE-Primary B-Cells;
NIH MGC Project;
Submitted (DEC-2001) to
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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Q6PJA4;
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mes 227; Conserv
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Pred. No. 4
                                                                                                                                                               99:16899-16903 (2002) .
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EMBL/GenBank/DDBJ databases

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Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

A Fobo G., Han M., Wiemann S.;

L Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.

REMBL; BX64067; CAR45781.1; -; mRNA.

REMBL; BX64067; CAR45781.1; -; mRNA.

RINterPro; IPR00359; IG.

RINterPro; IPR00359; Ig.

RINterPro; IPR003597; Ig.C1.

RINterPro; IPR003597; Ig.C1.

RINterPro; IPR003597; Ig.C1.

RINterPro; IPR003596; IG.MHC.

RINterPro; IPR003596; IG.

REMART; SM00406; IG.

REMART; SM00406; IG.

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REMBL/GenBank/DDBJ databases.

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REMBL/GenBank/DDBJ databases.

REMBL; SMART; SM00406; IG.; 1.

REMBL; SMART; SM0406; IG.; 1.

REMBL; SMART;
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InterPro; IPR00310; Ig-like.
InterPro; IPR0031597; Ig-cl.
InterPro; IPR003597; Ig_MHC.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP07654; Cleet; 3.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_MHC; UNKNO SEQUENCE 470 AA; 51716 MW;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence up
05-JUL-2004 (TrEMBLrel. 27, Last annotation
Hypothetical protein DKFZp686P15220.
Name=DKFZp686P15220;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The German cDNA Consortium;
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8
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MW; 7B49556A11FD7D99 CRC64;
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Pred. No. 4.3e-91;
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A GAUCHEY C., Klein P., Beliard R.;

Gaucher C., Klein P., Beliard R.;

T "Sequence determination of the recombinant human anti-RhD m

T antibody T125.";

L Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; AY894992; AAW82028.1; -; mRNA.

R Interpro; IPR003599; Ig.

R Interpro; IPR003597; Ig. C1.

R Interpro; IPR003597; Ig. C1.

R Interpro; IPR003597; Ig. C1.

R Interpro; IPR003597; Ig.

R Interpro; IPR003596; Ig.

Pfam; PF07664; C1-set; 3.

R Pfam; PF07665; V-set; 1.

NR Pfam; PF07665; V-set; 3.

NR Pfam; PF07666; V-set; 3.

NR SMART; SM00409; IG. 2.

NR SMART; SM00407; IGC1; 3.

SMART; SM00407; IGC1; 3.

SMART; SM00407; IGC1; 3.
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Best Local S
Matches 227
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Q5EFE5_F
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10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Anti-RhD monoclonal Ti25 gammal heavy chain precursor.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
                                                                                                                                                                                                                                                                                                                                                                                         Signal.
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
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                                                                                                                                            DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
  GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                            52362 MW;
                                                                                                                                                                                                                                              91.9%; Score 1233; DB 2;
100.0%; Pred. No. 4.4e-91;
tive 0; Mismatches 0;
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Pred. No. 4.4e-91;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                  Potential.
anti-RhD monoclonal T125
chain.
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausmer R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Guy L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gubbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Fahey J., Holton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length human

and monase conna secmences ":
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                                                                                                              Query Match
Best Local Similarity
Matches 227; Conser
                                                                                                                                                                                                                                                                Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

RMBL; BC073782; AAH73782.1; -; mRNA.

GO; GO:0016021; C:integral to membrane; IEA.

R InterPro; IPR003599; Ig.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR003597; Ig_Cl.

R InterPro; IPR003596; Ig_WHC.

R InterPro; IPR003596; Ig_WHC.

R InterPro; IPR003596; Ig_Y.

R Ffam; PF07654; Cl-set; 3.

R SMART; SM00409; IG; 2.

R SMART; SM00409; IG; 1.

R PROSITE; PS00359; IG_MHC; UNKNOWN_2.

W HYDNOTHERICAL TRANSFERS.
                                                                                                                                                                                                                            Hypothetical SEQUENCE 4:
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Proc. Natl. Acad. Sci. U.S.
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Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
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475 AA; 5
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                                                                                                           Conservative
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                                                                                               91.9%; bu
100.0%; Pr
'''a 0;
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Last sequence update)
Last annotation update)
                                                                                                        Score 1233; DB 2;
Pred. No. 4.4e-91;
0; Mismatches 0;
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      Query Match
                                                                                                                                                                                            InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_MCC.
InterPro; IPR003596; Ig_W.
InterPro; IPR003596; Ig_V.
Pfam; PF07554; Cl. set; 3.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ
EMBL; BC07373; AAH73773.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc.
                                                                                               PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Spleen;
MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein. Homo sapiens (Human).
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05-JUL-2004 (TrEMBLrel.
                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Spleen,
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Mammalia; Eutheria;
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                                                                    11 protein.
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                                                                    52286 MW;
      91.9%; Score 1233;
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Length 476;
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RESULT
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REMBLY APA727714, AAKSB686.2; - mRNA.

RMS: Q96PQ8; 39-180, 191-444, 447-679.

RMR: Q96PQ8; 39-180, 191-444, 447-679.

REBBEMBL; ENSGODO0057593; Homo sapiens.

GO; GO:0005505; F:cealcium ion binding; IEA.

GO; GO:0005505; F:cealcium ion binding; IEA.

GO; GO:0004253; F:chymotrypsin activity; IEA.

GO; GO:0004255; F:trypsin activity; IEA.

GO; GO:0004255; F:trypsin activity; IEA.

GO; GO:0006506; P:proteolysis and peptidolysis; IEA.

INTERPRO; IPR000152; Asx hydroxyl_S.

INTERPRO; IPR000152; Asx hydroxyl_S.

INTERPRO; IPR000148; EGF_Ca.

INTERPRO; IPR00148; EGF_Iike.

INTERPRO; IPR00148; EGF_Iike.

INTERPRO; IPR00148; EGF_Iike.

INTERPRO; IPR00130; EGF_Iike.

INTERPRO; IPR003597; Ig_Cl.

INTERPRO; IPR003597; Ig_Cl.

INTERPRO; IPR003597; Ig_Cl.

INTERPRO; IPR00354; Peptidase_SIA.

INTERPRO; IPR001314; Peptidase_SIA.

INTERPRO; IPR001254; Peptidase_SIA.

Pfam; P97654; Cl-set; 2.
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                    Pfam; PR07654; C1-set; 2.

Pfam; PF000594; Gla; 1.

Pfam; PF00089; Trypsin; 1.

Pfam; PF00722; CTYMOTRYPSIN.

PRINTS; PR00701; EGFBLOOD.

PRINTS; PR00001; GGABLOOD.
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Q8 HUMAN
Q96PQ8 HUMAN 1
Q96PQ8;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Factor VII active site mutant immunoconjugate.
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
Hu Z., Garen A.;
Submitted (FEB-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Targeting tissue factor on tumor vascular endothelial cells and cells for immunotherapy in mouse models of prostatic cancer."; Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hu Z.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606
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Catarrhini; Hominidae;
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SMART; SM000407; IGc1; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00010; ASX HYDROXYL; UNKNOWN_1.

PROSITE; PS010186; EGF_1; UNKNOWN_1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS00011; GLA_1; UNKNOWN_1.

R PROSITE; PS00013; GLA_2; 1.

R PROSITE; PS0098; GLA_2; 1.

R PROSITE; PS0098; GLA_2; 1.

PROSITE; PS00290; IG_MIC; UNKNOWN_1.

JR PROSITE; PS00290; IG_MIC; UNKNOWN_1.

DR PROSITE; PS00134; TRYPSIN_DOM; 1.

DR PROSITE; PS00135; TRYPSIN_DOM; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.
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C TISUB-Peripheral Nervous System;

X MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X MEDLINE=22388257; PubMed=12477932;

X Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F.,

XA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F.,

XA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

XA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.

XA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Wullahy S.J.

XA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Wullahy S.J.

XA Brownstein M.J., Watternan K.J., Malek J.A., Gunaratne P.H.,

XA Richards S., Morley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.

XI Blalon D.K., Muzny D.M., Sodergren B.J. Lu X., Gibbs R.A.,

XA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

XA Blakesley R.W., Touchman J.W., Goreen B.D., Dickson M.C.,

XA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

XA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

XA Schnerch A., Scheil J. P.J., Jones S.J.M., Marra M.A.,

XA Book M. J., Scheil J. J., Jones S.J.M., Marra M.A.,

XA Book M. J., Jones S.J.M., Marra M.A.,

XA Book M. J., Jones S.J.M., Marra M.A.,

XA Book M. J., Jones S.J.M., Marra M.A.,
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Q6P055;
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05-JUL-2004 (7
05-JUL-2004 (7
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05-70L-2004 (TREMBLrel. 27, Last annotation update)
19-70L-2004 (TREMBLrel. 27, Last sequence update)
19-70L-2004 (TREMBLrel. 27, Last seque
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Pred. No. 7e-91;
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                                                                                                                                                                                                                               range C.,
fullahy S.J.,
ratne P.H.,
Hulyk S.W.,
                                                                                                                                                                             Sanchez A.
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REMBL; BC065820; Ig.

REMBL; BC003599; Ig.

REMBC; IPR003599; Ig.

REMBC; IPR003599; Ig.

REMBC; IPR003596; Ig.

REMBC; IPR003596; Ig.

REMBC; SM00409; IG; 2.

REMBC; SM00409; IG; 2.

REMBC; SM00409; IG; 3.

REMBC; SM00409; IG; 1.

REMBC; SM00409; IG; 1.

REMBC; SM00406; IGV; 1.

REMBC; SM00406; IGV; 1.

REMBC; PS50035; IG_LIKE; 4.

REMBC; PS50035; IG_LIKE; 4
                                                                                                                                                                                                          TISSUE-Esophagus tumor;
The German cDNA Consortium;
Bahr A., Lauber J., Mewes H.W
Han M., Wiemann S.;
Submitted (JAN-2005) to the El
EMBL; EX640947; CAE45972.1;
                                                                                         InterPro; InterPro;
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      InterPro;
InterPro;
                                                                                                                                                         SMR;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation updat
Hypothetical protein DKFZp686G11190.
Name=DKFZp686G11190;
                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                InterPro;
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HUMAN
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Q6MZQ6; 20-475.
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      IPR003597;
IPR003006;
IPR003596;
                                                                                         IPR003599;
IPR007110;
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l. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Ig-like.
Ig_cl.
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99.6%;
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Pred. No. 9.2e
0; Mismatches
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Query Match 91.6%;
Best Local Similarity 99.6%;
Matches 226; Conservative
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Best Local (
                                                                                    Interpro; IPR007110; Ig-like.
Interpro; IPR007110; Ig-like.
Interpro; IPR003597; Ig_c1.
Interpro; IPR003597; Ig_wC.
Interpro; IPR003596; Ig_w.
Pfam; PF07654; C1-set; 3.
SMART; SM00409; IG_c1; 3.
SMART; SM00409; IGC1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS050835; IG LIKE; 4.
PROSITE; PS05099; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 480 AA; 52612 MW; 225247F
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SMART; SM00409; IG; 2.

SMART; SM00407; IGc1; 3.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS50835; IG_MHC; UNKNOWN_2.

PROSITE; PS00290; IG_MHC; UNKNOWN_2.

Hypothetical protein.

SEQUENCE 475 AA; 52043 MW; B7EAE25
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05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
Hypothetical protein DKF2
Hypothetical protein DKF2
Name=DKFZp686001196;
                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB=Bsophagus tumor;
The German cDNA Consortium;
Wambutt R., Heubner D., Mewes
Fobo G., Han M., Wiemann S.;
Submitted (JAN-2005) to the EN
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Eukaryota; Metazoa; C
Mammalia; Eutheria; E
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P01861; 1ADQ.
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Euarchontoglires; Primates; Catarrhini; Homi
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99.6%;
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el. 27, Last sequence update)
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el. 27, Dast annotation updat
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Score 1229; D
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Search completed: April 4, 2006, 13:15:18 Job time : 188.806 secs	434 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 480	182 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHBALHNHYTQKSLSLSPGK 228	374 GOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTPPVLDS 433	122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 181	314 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 373	62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121	254 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 313

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Result
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Listing first 45 summaries
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Maximum DB
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1: geneseqp1980
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Match
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1341
 2443163 seqs, 439378781 residues
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VEGF anta
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Human TAC
Vector 20
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28-	27	26	25
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Aeb46699	Aeb46697	Abj38341	Abj38333	Abj38338	Adc98568	Adc98586	Adc98588	Adc98614	Adc98592	Adc98590	Adc98594	Adc98596	Adc98598	Adw97969	Aae15489	Aab16966	Aea18571	Abb73416	Aab16965	Abb73426
	Human FSH	TALL-1	TALL-1 i	TALL-1 i	Human ang	Human TWE	Mouse BCM	EMP-EMP-F	Amino aci	EPO mimet	EMP-Fc pr	MMP inhib								

ALIGNMENTS

AAB16961 standard; protein; 247

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Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; immetic; IL-1; TNF; antagonist; Minhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; vascular endothelial growth factor; matrix metalloproteinase; Homo sapiens. Synthetic. 31-OCT-2000 23-OCT-1998; 22-OCT-1999; 25-OCT-1999; 04-MAY-2000. WO200024782-A2 thrombosis; pharmaceutical. TMP-Fc protein sequence SEQ ID NO:12. AAB16961; (AMGE-) AMGEN INC. (first entry) 98US-0105371P 99US-00428082 99WO-US025044. MY D

The present invention describes composition of matter (I) comprising Fc domain, pharmacologically active peptides, and linkers. Where (I) $(X1)_{A}-F1-(X2)_{b}$, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1,

P2

Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.

21; Page 188-189; 608pp; English.

N-PSDB;

AAA69447

WPI; 2000-350702/30.

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Cheetham

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RESULT 2
ABB73414
ID ABB73414
AC ABB7
XX ABB7
XX ABB7
XX ABB7
XX ABB7
XX Modi
KW MMP
KW TNP-
KW TNP-
KW TNP-
KW TNP-
KW TNP-
KW TNP-
KW Cytc
KW TNP-
KW Cytc
KW TNP-
KW Cytc
KW Fanc
KW Canc
KW Selee
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                                                                                                                                                                                                                                                                                                          Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor; TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP; TPO mimetic peptide; EPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antirheumatic; antiarthritic; antidiabetic; dermatological; neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 247 AA;
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                             02-MAY-2001; 2001WO-US014310
                                                                                     08-NOV-2001
                                                                                                                                  WO200183525-A2
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                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                    thrombocytopaenia; metastatic tumour; systemic lupus erythematosus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TMP-Fc amino acid SEQ ID NO:12.
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cc neuroprotective activities. (I) can be used as a therapeutic or prophylactic agent as well as for screening purposes. (I) is useful for cdiagnosing diseases characterised by dysfunction of their associated cc protein of interest, for identifying normal or abnormal proteins of interest, as a part of diagnostic kit to detect the presence of their compounds are useful autoimmune diseases, tumour growth, cancer, rheumacoid arthritis, diabetic retinopathy, obesity, sleep disorders, compounds are useful for treating disorders, the compounds are useful for treating disorders characterised by low red blood cell levels such as anaemia. The TPO-mimetic compounds are useful for treating conditions that involve an existing megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777 represent amino acid and nucleic acid sequences used in the
  Query Match
Best Local S
Matches 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a vehicle-peptide molecule (I) or its multimers. (I) can have antiinflammatory, antitumour, immunosuppressi cytostatic, antitheumatic, antitiabatic ophthaimologi antianaemic, anorectic, antiinfertility, haemostatic, dermatological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
                                                                                  Sequence 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 21; Fig 10; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABL35764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAY-2000; 2000US-00563286
                                                                                                                           exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diabetic retinopathy, obesity, sleep disorders and infertility.
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    247;
                       Similarity
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    Conservative
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100.0%; Score 1341; DB 5; 100.0%; Pred. No. 5.6e-93; tive 0; Mismatches 0;
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    Indels
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RESULT 3
AAB16960
ID AAB1
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               31-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                         1 MIEGPTLROWLAARAGGGGGDKTHTCPPCPAPELLGGPSVFLFPPKRKDTLMISRTPEVT
                                                                                                                                                                                                                                                                                                                                                        1 MIEGPTLROWLAARAGGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
                                                                                                                                                                                                                                                                                                                  CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
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               (first entry)
                                                                  protein;
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                                                                                                                                                                                            VMHEALHNHYTQKS
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TMP-TMP-Fc

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The present invention describes composition of matter (I) comprising an CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is: CC (X1)a-F1-(X2)b, where: Fl = an Fc domain; X1 and X2 = are each cach cC (X1)a-F1-(X2)b, where: Fl = an Fc domain; X1 and X2 = are each cC (X1)a-F1-(X1)c-F1-(X1
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Matches 246
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22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibitor; erythropoietin; thrombopoietin; interleukin
cytotoxic T cell lymphocyte antigen 4; tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mmunosuppressive; EPO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246;
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ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
                                                                                                                                         KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW
                                                                                                                                                                                                                                        VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
                                                                                                                                                                                                                                                                                  VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKĖYKC
                                                                                                                                                                                                                                                                                                                                                                                                                        IEGPTLRQWLAARAGGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC
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                                                                                                      KVSNKALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEW
                                                                                                                                                                                                                                                                                                                                                                          IEGPTLRQWLAARAGGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC
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SPO; TPO; CTLA4; mimetic; IL-1; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1336; DB 3;
; Pred. No. 1.5e-92;
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c; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombolytic; VEGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive, CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological, CC antianemic, anorectic, antiinfertility, haemostatic, dermatological and correctorive activities. (I) can be used as a therapeutic or comproprotective activities. (I) can be used as a therapeutic or components of interest, for identifying normal or abnormal proteins of interest, for identifying normal or abnormal proteins of interest, for identifying normal or abnormal proteins of compounds are useful for creating inflammatory and autoimmune diseases, tumour growth, cancer, infertility, and neurological degenerative diseases, tumour growth, cancer, compounds are useful for treating disorders characterised by low compounds are useful for treating conditions that involve an existing compounds are useful for treating conditions that involve an existing deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic cumour which result in thrombocytopaenia, svaremic immune metastatic
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                                                                                                                                                                                                                                                                                                                                                                        Example 2; Fig 9; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-)
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DB; ABL35763.
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Pred. No. 1.5e-92;
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                                                                                                                                                                                                                                                                                             TWEAK protein; TREPA; Apo3L; TWEAK receptor; radiotherapy; chemotherapy; pharmaceutical; delivery mechanism; antagonist; anglogenesis inhibition; transgenic animal; transgenic plant; protein interaction; animal disease model; angiogenesis disorder; antiangiogenic; solid tumor cytostatic; neoplasm; opthalmological; inflammation; antiinflammatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New fusion proteins comprising multimeric soluble TWEAK receptor fragments and an oligomerization domain, useful for antagonizing receptor or for treating diseases mediated by anglogenesis, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
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99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1270;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           compositions relating to
le fragments of the major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 275;
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solid
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Matches 234;
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides methods and compositions relating to fusion proteins comprising multimeric soluble fragments of the major functional TWEAK (also called TREPA and Apoll) receptor (TWEAKR) and an oligomerization domain. The invention is useful for inhibiting angiogenesis and for treating diseases such as solid tumors, ocular neovascularization and inflammatory conditions. The TWEAK receptor proteins of the invention are also used in the production of transgenic animals and plants. The present sequence is human TWEAK receptor (TWEAKR) - Gly5 - TWEAKR - Gly5 - IGG1 Fc portion fusion protein. This fusion protein comprises a N-terminal methionine residue, human TWEAKR, pentaglycine linker and the Fc portion of human IGG1 where the TWEAKR, pentaglycine linker and the Fc portion of the SEQ ID NO: 7. This sequence is used to illustrate an ELISA-setyle assay useful for determining the hinding to hinding the sequence is used to illustrate an ELISA-setyle assay useful for determining the hinding to hinding the manner.
                                                                                                                                                                                                                                                                                                                                            Sequence 322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 40; SEQ ID NO 19; 140pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion proteins comprising multimeric soluble TWEAK receptor fragments and an oligomerization domain, useful for antagonizing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
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   268
                                 193
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                                                                                                                                                                                                                                                                                                                                                                                               assay useful
                                                                                                                                                                     73
                                                                                                                                                                                                      88
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                                                                                                                                                      VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 132
                                                                                                                                                                                                                        ARAGGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
                                                                                     EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 192
TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 322
                       TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSBGK 247
                                                                 EKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYK
                                                                                                                                 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
                                                                                                                                                                                                     AAAGGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammation.
                                                                                                                                                                                                                                                                          Conservative
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                            for determining the binding properties of TWEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 90
                                                                                                                                                                                                                                                                                      94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Pentaglycine linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Human TWEAK receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Pentaglycine linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Human IgG1
                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                      Score 1270; DB 9;
Pred. No. 1.7e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TWEAK receptor"
                                                                                                                                                                                                                                                                        Mismatches
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RESULT 7 ADW97943

Query Match

94.78;

Score 1270;

멂 9;

Length 339;

Sequence 339 AA;

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The present invention provides methods and compositions relating to the present invention provides methods and compositions relating to the major functional TWEAK (also called TREPA and Apoll) receptor (TWEAKR) and an collygemerization domain. The invention is useful for inhibiting and an collygemerization domain. The invention is useful for inhibiting angiogenesis and for treating diseases such as solid tumors, ocular convex collarization and inflammatory conditions. The TWEAK receptor convex cularization and inflammatory conditions. The TWEAK receptor contains of the invention are also used in the production of transgenic animals and plants. The present sequence is human TWEAK receptor (TWEAKR) contains and plants. The present sequence is human TWEAKR, this fusion protein. This fusion corresponds to residues 29 through 70 of the SEQ ID contains TWEAKR, pentaglycine linker and the Fc portion of human TWEAKR, linker, the TWEAK receptor corresponds to residues 29 through 70 of the SEQ ID contains sequence is used to illustrate an ELISA-style assay useful contains the binding properties of TWEAK binding molecules.
                                                                                                                                                                                                                                                                                  Claim 40; SEQ ID NO 18; 140pp; English
                                                                                                                                                                                                                                                                                                                                    New fusion proteins comprising multimeric soluble TWEAK receptor fragments and an oligomerization domain, useful for antagonizing receptor or for treating diseases mediated by angiogenesis, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-123128/13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWEAK protein; TREPA; Apo3L; TWEAK receptor; radiotherapy; chemotherapy; pharmaceutical; delivery mechanism; antagonist; angiogenesis inhibition; transgenic animal; transgenic plant; protein interaction; animal disease model; angiogenesis disorder; antiangiogenic; solid tumor; cytostatic; neoplasm; opthalmological; inflammation; antiinflammatory; fusion protein; immunoglobulin; igg; fc receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUL-2004; 2004WO-US023904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADW97943 standard; protein; 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TWEAKR:1KPEG:TWEAKR:Gly5:Fc fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2003US-0490036P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Pentaglycine linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Human TWEAK receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Transcription start site region (N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Human IgG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Human TWEAK receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Linker"
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                 The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. NNAs, vectors and host cells from the present invention can be used for producing pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; Minhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                   Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified peptide; therapeutic agent; fusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNF-alpha inhibitor-Fc fusion protein sequence SEQ
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                                                                                                                                                                                                                                                                                                                                             AAA69502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAGGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
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Novel vehicle-peptide molecule or its inflammatory and autoimmune diseases,

148

multimers useful for treating cancer, rheumatoid arthritis,

N-PSDB;

2002-130313/17. DB; ABL35770.

02-MAY-2001; 2001WO-US014310

03-MAY-2000; 2000US-00563286

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor; TNF-alpha inhibitor; interleukin 1 antagonist; TI-1 antagonist; TMP; TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; antianaemic; anorectic; antiinfertility; haemostatic; dermatological; neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; disbetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; anaemia; thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
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98.7%;
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No. 1.5e-87;
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches 234
                                                                                                                                   TALL-1-binding protein; IALL-1-binding protein; IALL-1-binding protein; IALL-1-binding protein; IALL-1-binding protein; IALL-1-binding protein; IALL-1-binding protein; B-cell-mediated cancer; lymphoma; inflammation; attheroscie pancreatitis; atheroscie; inflammation; osteoporosis; Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis; glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis; glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis; glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis;
                                                                                                                        gene
                                     WO200292620-A2
                                                                                                                                                                                                                                          TALL-1-binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a vehicle-peptide molecule (I) or multimers. (I) can have antiinflammatory, antitumour, immunosuppre
                                                                               Unidentified.
                                                                                                                                                                                                                                                                                         TALL-1 inhibitory protein SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                      ABJ38339 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 190
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98.7%;
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Pred. No. 1.5e-87;
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21-NOV-2002

glomerulonephritis;

Hashimoto's

TALL-1-binding protein; TALL-1; B-cell-mediated autoimmune disease; systemic lupus erythematosus; B-cell-mediated cancer; lymphoma; inflammation; rheumatoid arthritis; acute pancreatitis; atheroselerosis; Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis;

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RESULT 11
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                                                                                                                                                              TALL-1 inhibitory protein SEQ ID
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rematches 7;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis;
   12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                      Sequence 252 AA;
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                       ABJ38344;
                                           ABJ38344 standard; protein; 293
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                                                                                                                                        QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
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TALL-1 inhibitory protein SEQ ID No TALL-1; B-cell-mediated autoimmune disease; 123.

systemic lupus erythematosus; B-cell-mediated cancer; lymphoma; inflammation; rheumatoid arthritis; acute pancreattitis; atherosclerosis; Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis; glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis; multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis;

13-MAY-2002; 2002WO-US015273

11-MAY-2001; 2001US-0290196P

New TALL-1-binding polypeptide, useful for modulating the activity TALL-1 and in treating, preventing or diagnosing a B-cell-mediated autoimmune diseases, cancers or lymphomas.

68; 236pp; English.

The invention relates to a novel TALL-1-binding polypeptide comprising a defined sequence in the specification. The composition is useful in modulating the activity of TALL-1, and in treating, preventing, ameliorating, diagnosing or prognosing a B-cell-mediated autoimmune disease (e.g. systemic lupus erythematosus) or B-cell-mediated cancer or lymphoma. The composition may also be used in treating inflammations (e.g. rheumatoid arthritis), acute pancreatitis, Alzheimer's disease, asthma, atherosclerosis, cachexia, cirrhosis, diabetes, glomerulonephritis, Hashimoto's thyroiditis, lischaemic injury, multiple myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, psoriasis and vasculitis. Disorders may be treated with the novel composition using gene therapy. This sequence represents a TALL-1 inhibitory protein of the

94.6%; ω --Score 1268.5; Pred. No. 2e-Mismatches 26-87; DB 4. 6 Indels Length

66 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 7 LROWLAARAGGGGG-DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN IKQMVCDPLGGGGGVDKTHTCPPCPAPBLLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD EKTISKAKGQPREPQVYTLPP\$RDELTKNQVSLTCLVKGFYPSDIAVEWESNG 185 171 125 65 291

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                                                                                                                                                                                                                                                                                                                                                                            CC The present sequence is the protein sequence of AGP3 peptibody, an AGP3 CC trandem dimer peptide-Fc fusion. A claimed method for treating an CC inflammatory or an autoimmune condition comprises administering at least CC one of an AGP3 inhibitor, a BAFFR inhibitor and a TACI inhibitor CC comprising the present sequence, and at least one of a B7 inhibitor and a CC CD28 inhibitor. Alternatively, the AGP3 inhibitor or CC TACI inhibitor is used in combination with an interleukin-1 inhibitor or CC such as KLM2 ADD76791 or a tumour necrosis factor-alpha inhibitor such as CC STMFR-1 ADD76792. The AGP3 inhibitor prevents binding of AGP3 to BAFFR CC and TACI. The inflammatory or autoimmune condition is selected from CC rheumatoid arthritis, psoriatic arthritis, systemic lupus erythematosus, CC graft rejection, psoriasis and inflammatory bowel disease. In examples CC graft rejection, psoriasis and inflammatory bowel disease. In examples CC graft rejection, psoriasis and inflammatory bowel disease. In examples CC graft rejection, psoriasis and inflammatory bowel disease. The camples CC graft rejection psoriasis and inflammatory bowel disease. The camples CC graft rejection compared to KIN2 or STMFR-1 and AGP3 peptibody reduced collagen-induced arthritis in susceptible B10.RIII mice for an CC extended period compared to KIN2 alone.
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Best Local S
Matches 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating an inflammatory, or autoimmune condition, e.g interleukin-1 or tumor necrosis factor-alpha comprises administering an IL-1 or TNF-alpha inhibitor and at least one of a B7 inhibitor and a CD28 inhibitor.
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 69; SEQ ID NO 1; 203pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-534365/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-DEC-2002; 2002US-0437405P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-DEC-2003; 2003WO-US041378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004060911-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   co-stimulatory factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGP3; peptibody; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ76789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ76789 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .mmunosuppressive; dermatological;
                                                                                                                                                                                                                                                                                              Local Similarity
                        186
                                                          172
                                                                                                                                112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptibody, useful in
                                                                                            126
                                                                                                                                                                  99
                                                                                                                                                                                                      52
                                                                                                                                                                                                                                          7
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                     LRQWLAARAGGGGG-DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
                                                                                                                                                                                                                                                                                                                                                 293 AA;
                                                      KALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNG
                                                                                 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG
                                                                                                                            VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
                                                                                                                                                              VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
                                                                                                                                                                                                    IKQWVCDPLGGGGGVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                           94.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293
                                                                                                                                                                                                                                                                                       Score 1268.5; DI
Pred. No. 2e-87;
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and inflammatory disease therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      combination therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiarthritic; antipsoriatic;
                                                                                                                                                                                                                                                                                                             BB
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                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                             293;
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                                                                                                                                                                                                                                                                          Gaps
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RESULT 14
AAB17956
ID AAB17956
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AU
                                                                    CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(C2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               맑
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        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes composition of matter (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; Minhbitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; cysotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 6; Page 582-583; 608pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; therapeutic agent; fusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu
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99US-00428082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boone TC;
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Best Local Similarity Matches 233; Conserv

Conservative

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94.5%;

Score 1267; DB Pred. No. 2.2e-8

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Length 252; Indels

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Gaps

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ed. No. 2.2e-87; Mismatches 1

Query Match

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RESULT 15
ABB73424
ID ABB73424
ID ABB73424
ID ABB73424
ID ABB73424
AC ABB73
XX MOdif
KW MWP1;
FW MO200
XX Fance
XX Homo
OS Synth
XX PANCO
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                                        The present invention describes a vehicle-peptide molecule (I) or its multimers. (I) can have antiinflammatory, antitumour, immunosuppressive, cytostatic, antiirheumatic, antiarthritic, antiidabetic, ophthalmological antianaemic, anorectic, antiinfertiilty, haemostatic, dermatological and neuroprotective activities. (I) can be used as a therapeutic or prophylactic agent as well as for screening purposes. (I) is useful for diagnosing diseases characterised by dysfunction of their associated protein of interest, for identifying normal or abnormal proteins of interest, as a part of diagnostic kit to detect the presence of their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor; TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP; TPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antirheumatic; antiarthritic; antiidabetic; ophthalmological; antianaemic; anorectic; antiinfertility; haemostatic; dermatological; neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                               Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-2002
                                                                                                                                                                                                                                                                                                                                                                      Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002-130313/17.
)B; ABL35774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antagonist-Fc fusion nucleic acid SEQ ID
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Matches 233
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                                                                                                                                                                                                                                                                                                                                                                Sequence
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Ig gamma-3 chain C
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Ig gamma-2 chain C
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ALIGNMENTS

RESULT S31866

RESULT 2 GHHU Ig gamma-1 chain C region - human C;Species: Homo sapiens (man) C;Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004 C;Accession: A93433; S35861; S33887; B99563; A90564; B91668; A91723; A02146 C;Accession: A93433; S35861, Food, L.E. R;Ellison, J.W.; Berson, B.J.; Hood, L.E. Nucleic Acids Res. 10, 4071-4079, 1982 A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene. A;Reference number: A93433; MUID:82274238; PMID:6287432 A;Molecule type: DNA	Qy 141 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 200	SRTPEVTCVVVDVSHEDPEVKFNWYVD 80	A;Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PC;Keywords: immunoglobulin F;1-22/Region: Bscherichia coli outer membrane protein A precursor F;23-255/Region: human Ig gamma-1 chain C region Query Match Best Local Similarity 100.0%; Pred. No. 5.3e-88; Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Ig gamma-1 chain C region - synthetic G;Species: synthetic A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000 C;Accession: S31866 R;Filpula, D. Submitted to the EMBL Data Library, February 1993 A;Description: Screeing method for protein-protein interactions of cloned gene product A;Reference number: S31866 A;Accession: S31866 A;Rosiedes: 1-255 <fild 1-255="" <fild<="" a;residues:="" td=""></fild>

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A,Molecule type: protein
A,Residues: 1-96, R', 98-135 <CUN>
A,Residues: 1-96, R', 98-135 <CUN>
A,COOSE-references: UNIPARC: UPI000017378D
A,Ote: this sequence has the GIm(3) marker, 97-Arg
A,Note: this sequence has the GIm(3) marker, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A,Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid
A,Reference number: A90564; MUID:71064025; PMID:5530842
A,Contents: Eu
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A;Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370
A;Note: this sequence has the Gim(17) allotypic marker, 97-Lys, and the
                                                                                                                                      A;Contents: annotation; disulfide bonds R;Dreker, L; Schwarz, J.; Reichel, W; Hilschmann, N. R;Dreker, L; Schwarz, J.; Reichel, W; 515-1540, 1976 Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976 A;Title: Rule of antibody structure. The primary structure enbromide cleavage products, and the disulfide bridges. A;Reference number: A91667, MUID:77070267; PMID:1002129
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A; Molecule type: protein
A; Residues: 1-96,'K',98-197,'D',199-238,'B',240,'M',242-266,'D',268-271,'D',273-330
A; Cross-references: VIPI0000173790
A; Cross-references: Company of the Company of the Sequence has the Glm(3) and Glm(non-1) markers
A; Note: this sequence has the Glm(3) and Glm(non-1) markers
R; Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
Biochemistry 9, 3188-3196, 1970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Contents: myeloma protein Nie
A;Accession: B91668
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A;Accession: protein
A;Residues: 1-34, Q',36-96, K',98-115, 'Q',117-197, 'D',199-238, 'D',240, 'L',242-268, 'E',27
A;Cross-references: UNIPARC:UPI000017378F
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A;Molecule type: DNA A;Residues: 88-113/235-330 <TAK>
A;Residues: Reference reviews and control of the control
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A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E'
A;Cross-references: UNIPARC:UPI000017378B
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A;Gene:
                                                   A; Contents: annotation; C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: The covalent structure of a human gammaG-immunoglobulin. A; Reference number: A90565; MUID:71064027; PMID:4923144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A90564
A; Molecule type: pr
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A;Reference number: S33904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Harris
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Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo,
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PMID:6811139
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A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14432.33-14432.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C;FC;Copyonain; immunoglobulin homology <IM1>
E;20-85/Domain; immunoglobulin homology <IM1>
                                                                                                                                                                                                                                                                                                                                                     R;Khamlichi, A.A.
submitted to the EMBL Data
A;Reference number: $72664
A;Accession: $72664
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A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
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A; Residues: 1-374 < KHA>
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B
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A; Residues: 1-140,'C',142-374 <KH2>
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Best Local S
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                          GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
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                                                                                                    DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
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100.0%; Pr
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Pred. No. 2.5e
2; Mismatches
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Pred. No. 7.4e-88;
0; Mismatches 0;
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Ig gamma chain C region - chimpanzee
C;Species: Pan trogLodytes (chimpanzee)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-
C;Accession: PT0207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc
A;Reference number: PT0207; MUID:91287716; PM
A;Accession: PT0207
A;Molecule type: mRNA
A;Residues: 1-234 CEHR>
                                A;Map position: 14932.33-14932.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin C;Keywords: immunoglobulin
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C;Superfamily: immunoglobulin C region; immunog
C;Keywords: immunoglobulin
F;48-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                         A; Cross-references:
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A; Residues: 1-377 < HUC>
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Query Match
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                                                                                                                                                       UNIPARC: UPI000004718F;
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  85.5%;
92.5%;
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Pred. No. 5.9e
1; Mismatches
 Score
Pred.
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 1146; DB 2;
No. 4.6e-81;
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PMID:2062315
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RESULT
G2HU
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A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:Q8N4Y9; UNIPARC:UPI0000176F0B
A;Cross-references: UNIPROT:Q8N4Y9; UNIPARC:UPI0000176F0B
C;Superfamily: immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, A;Reference number: A60764; MUID:90007613; PMID:2571587 A;Accession: A60764
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Huck, S.; Lefranc, G.; Lefranc,
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision
C;Accession: A60764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig gamma-3
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Best Local Similarity
Matches 210; Conserv
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                                                                                                                                                                                                            GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 140
                                                             DGSFFLYSRLTVDKSRWQEGNVPSCSVMHEALHNRFTQKSLSLSPGK
                                                                                 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                                                                                                                                                                                                                                                                                        DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
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Pred. No. 6.5e-81;
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R;Ellison, J.; Hood, L.
Proc. Natl Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>

UNIPROT: P01859;

UNIPARC: UPI000003BFCC;

GB:V00554; GB:J00230;

NID

ά

Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change
C;Accession: A9306; A92809; A90752; A93132; A02148

09-Jul-2004

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Biochem. J. 121, 217-225, 1971

A;Title: Disulphide bridges of the heavy chain of human A;Reference number: A90253; MUID:72033500; PMID:4940472

A;Contents: annotation; myeloma protein Sa, disulfide bor R;Frangione, B.; Milstein, C.; Pink, J.R.L.

Nature 221, 145-148, 1959

A;Title: Structural studies of immunoglobulin G.

A;Reference number: A93157; MUID:69064124; PMID:5782707

A;Contents: annotation; Sa, disulfide bonds

C;Genetics:
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A;Gene: GDB:IGHG2

A;Cross-references: GDB:119338; OMIM:147110

A;Cross-references: GDB:119338; OMIM:147110

A;Map position: 14q32.33-14q32.33

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;30-85/Domain: immunoglobulin homology <IMI>
F;30-85/Domain: immunoglobulin homology <IMI>
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A;Accession: A93132
A;Accession: A93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
A;Cross-references: UNIPARC:UPI0000173794
R;Hofmann, T.; Parr, D.M.
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A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24, 'E', 26-57, 'EV', 60-85;112-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196,'Q', 198-A;Residues: 1-24, 'E', 26-57, 'EV', 60-85;112-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196,'Q', 198-A;Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The primary structure of a human 1 A;Reference number: A92809; MUID:81007873; A;Contents: myeloma protein Til A;Accession: A92809
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A;Cross-references: UNIPARC:UPIO000173791
A;Note: Trp-156 is at or near the complement-binding site of the complement of the comple
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A;Contents: annotation; Zie,
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Matches 209
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Immunol. 16, 923-925
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J. Biochem. 57, 758-767, 1979
                                                                                                                                                                                                                                                                                                         Local Similarity
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          165
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                                                                        NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
                                                                                                                                                                                                                                                                                                                                                                                                          site: carbohydrate (Asn) (covalent) #status predicted
      NAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPRE
                                                                                                                                      CPPCPAPP-VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVH
                                                                                                                                                                                                 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
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                                                                                                                                                                                                                                                                                                     Score 1142.5; DB Pred. No. 7.1e-81;
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    PMID:6774012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: GDB:IGHG4
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TQKSLSLSPGK
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A;ACCEBBACH. A;ACCEBBACH. A;ACCEBBACH. A;MOLOCULE type: DNA A;Residues: 1-327 <ELL> A;Residues: 1-327 <ELL> A;COBS-references: UNIPROT:P01861; UNIPARC:UPI0000047190 A;COBS-references: UNIPROT:P01861; UNIPARC:UPI000047190 A;Note: the sequence was determined from the germline gene R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C. Biochem, J. 117, 33-47, 1970 Biochem, J. 117, 33-47, 1970 A;Title: Human immunoglobulin sublclasses. Partial amino ac a;Title: Human immunoglobulin sublclasses. Partial amino ac a;Title: Human immunoglobulin sublclasses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;99-110/Region: hinge
F;99-110/Region: hinge
F;934-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;27-83,141-201,247-305/Disulfide bonds: #status chain) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light C;Complex: An immunoglobulin beterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology <IMI>
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C;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
C;Dates: 01-Apr-1983; A90249; A02150
C;Accession: A9033; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
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A; Residues: 1-30;81-326 < PIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;106,109/Disulfide bonds: interchain F;177/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796
C;Genetics:
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IAVEWESNGOPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHY
                                              IAVEWBSNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
                                                                                                                                                                                                                                                                                                                                           PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
                                                                                                                                                                                                                                                                                                                                                                                                                   GTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDKTHT------CPPCPAPELLGGPSVFLFPPKPKDTLMISRT
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                                                                                                                                       KEYKCKVSNKGLPSSIEKTI
                                                                                                                                                                                                    KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD
                                                                                                                                                                                                                                                                    PEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1135.5;
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O
                                                                                                                                       PREPOVYTLPPSQEEMTKNQVSLTCLVKGFYPSD
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PMID:4192699
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TQKSLSLSLGK

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A;ROLECULE: 1-289 <FRA>
A;Residues: 1-289 <FRA>
A;Cross-references: UNIPARC:UPI0000173797
A;Cross-references: UNIPARC:UPI0000173797
A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 cd
A;Note: the sequence of residues 42-76 was taken from the reference that follows

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A;Note: the sequence of residues 42-76 was taken from the reference that follows

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A;Note: the sequence of residues 42-76 was taken from the reference that follows

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A;Note: the sequence of residues 42-76 was taken from the reference that follows
                                                                                                                                                                                                                           C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid F;203-270/Domain: immunoglobulin homology <IMM> F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: this sequence
C; Comment: The heavy c
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
A;Cross-references: UNIPARC;UPI0000173799
A;Note: this protein lacks most of the V region, all of the R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: Cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C. Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein A;Reference number: A90198; MUID:77021516; PMID:823945
A;Contents: heavy chain disease protein Zuc, partial sequence corr
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                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-15'
A;Cross-references: UNIPARC:UPI000017379A; UNIPARC:UPI000017379B; UNIPARC:UPI000017379C
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A;Title: Primary structure of the 'hinge' region of human A;Reference number: A92219; MUID:77118561; PMID:402363

A;Contents: normal gamma-3 chains, sequence corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: a carboxyl-terminal Lys is removed posttranslationally A; Note: this sequence may represent an allelic form or another C; Comment: The heavy chain disease protein Wis is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A93915; MUID:82247835; A;Contents: heavy chain disease protein Omm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: gamma heavy chain disease in man: cDNA sequence supports A;Reference number: A93915; MUID:82247835; PMID:6808505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein A; Residues: 12-97 < MIC>
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                                                                                                                                                                                                                                                                                                                                                                                   A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GDB:119339; OMIM:147120
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: GDB:IGHG3
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A;Note: the hinge region in gamma-3 chain
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C;Species:
64
                                                          21
                                                                                                                                              Similarity
                                           DKTHTCPPCPAPELLGGPSVFLFPPKKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                                                                                                                                                                                      14q32.33-14q32.33
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                                                                                                                                     83.6%;
                                                                                                               Score 1121; I
Pred. No. 2.8e
13; Mismatches
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                                                                                                               1.8e-79;
1es 9;
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A; Molecule type: protein
A; Rosidues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',2A; Residues: 129-131;155-172,'D',174-184,'A', 186,'E',188-200,'D',2A; Rross-references: UNIPARC:UPI00001737AD; UNIPARC:UPI00001737AB
A; Note: this has the e15 allotypic marker, 185-Ala
C; Complex: An immunoglobulin heterotetramer subunit consists of the hain disulfide bonds: In some cases, such as IgA and IgM, the subtraction disulfide bonds: In some cases, such as IgA and IgM, the subtraction disulfide bonds: Tresident of the subtraction of the sub
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A; Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 < MAR>
A; Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 < MAR>
A; Roross-references: UNIPARC:UPI000016C5ED; GB:M16426; NID:g165111; PIDN:AAA31289.1;
A; Note: this sequence has the dl1 allotypic marker, 104-Met, and the e15 allotypic marker.
A; Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A; Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobu A; Reference number: A90245; MUID:70110015; PMID:5461106
A; Recession: A90245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UPI00001737AC R;HILL, Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R. in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, A;Reference number: A94416 A;Recession: A94416
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A; Residues: 1-47,'E','49-71,'PV',72-128 <PRA>
A; Cross-references: UNIBARC: UDI00001737AB
A; Cross-references: UNIBARC: UDI00001737AB
R; Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Kn
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1992
A; Title: Heavy chain genes of rability IgG; isolation of a
A; Reference number: A93928; MUID:83299917; PMID:6193512
A; A; Accession: A93928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Pratt, D.M.; Mole, L.E.
Blochem. J. 151, 337-349, 1975
A;Title: Sequence studies on the constant region of the A;Reference number: A90290; MUID:76135469; PMID:1243651
A;Accession: A90290
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change
C;Accession: A91749; A90290; A39328; A90245; A94416; A02161
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A;Title: Nucleotide sequence of a rabbit IgG heavy chain from th
A;Reference number: A91749; MUID:84030930; PMID:6313520
A;Accession: A91749
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
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GHRB
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A; Residues: 132-143, 'E', 145-161 <FRU>
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                                        Query Match
Best Local
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28; Mismatches
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al Similarity 167; Conserv

Conservative

.7e-

<u>ن</u>

Gaps

<u>ب</u>

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Ig gamma 2a chain constant region - pig (fragment)
C.Species: Sus scrofa domestica (domestic pig)
C.Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #to
C.Accession: 147159
R.Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A.Title: Five putative subclasses of swine IgG identii
A.Reference number: I47158; MUID:95015845; PMID:793057
A.Accession: I47159
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Ressidues: 1-328 <KAC>
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R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG A;Reference number: I47158; MUID:95015845; PMI A;Accession: I47160
A;Status: preliminary; translated from GB/EMBL A;Molecule type: mRNA A;Residues: 1-328 <KAC-A;Cross-references: UNIPARC:UPI000011525; EMB C;Genetics: A;Genetics: A
                                                                                                                                                                                                                                                                                                                            RESULT
147159
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Best Local
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Pred. No. 7.6e
29; Mismatches
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PMID:7930579
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7.6e-63;
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     Ig gamma-2 chain C region - guinea pig C;Species: Cavia porcellus (guinea pig) C;Date: 07-May-1981 #sequence_revision
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A;Cross-references: UNIPARC:UPI0000115524; EMBL:U03779; C;Genetics: A;Gene: IgG2a A;Gene: IgG2a C;Superfamily: immunoglobulin C region; immunoglobulin F;133-202/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                              A;Gene: IgG4
C;Superfamily: immunoglobulin C region; :
F;82-151/Domain: immunoglobulin homology
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A; Residues: 1-277 < KAC>
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J. Immunol. 15
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DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 247
                                                                    GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVL
                                                                                                                   TKTKPPCPICPACEGPGPSAFIFPPKPKDTLMISRTPKVTCVVVDVSQENPEVQFSWYVD
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                                                  GQTREPQVYTLPPPTEELSRSKVTLTCLVTGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQ
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72.1%;
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Pred. No. 1.8e
29; Mismatches
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Pred.
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No. 7.6e-63;
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07-May-1981

#text_change

09-Jul-2004

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A;Contents: annotation; disulfide bonds
A;Note: Cys-16 is involved in a heavy-light chain bond
A;Note: Cys-16; Cys-107, and Cys-10 form inter-heavy chain bonds
A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin cregion; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C;Superfamily: immunoglobulin homology <IML>
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F;241-310/Domain: immunoglobulin homology <IM3>
F;28-79/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin. A;Reference number: A90354; MUID:71058474; PMID:4922544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 227-311 <TR2>
A;Cross-references: UNIPARC:UPI00001737A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Primary structure of the C-H3 homology region from A;Reference number: A90385; MUID:75036073; PMID:4609467 A;Accession: A90385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPARC:UPIO
R;Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A;Reference number: A90384; MUID:75036072; PMID:4429665
A;Accession: A90384
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A;Residues: 69-133;312-329 <TUR>
A;Cross-references: UNIPARC:UPI00001737A0; UNIPARC:UPI00001737A1
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Biochemistry 10, 9-17, 1971
A;Tille: Structure of heavy chain from strain 13 guinea pig
A;Reference number: A90359; MUID:71058486; PMID:5538616
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R;Birchtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III.
A;Reference number: A90352; MUID:71058471; PMID:5538606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 134-226 <TRA>
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                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;142-202/Disulfide bonds: #status experimental;178/Binding site: carbohydrate (Asn) (covalent);248-308/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;28-79/Disulfide bonds: #status experimental
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                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                     HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 144
EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDG 202
                                                            GNAETKPRVEQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPR
                                                                                                                                                                                                                                   TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
                                                                                                                                                                                      TCPKCPPPENLGGPSVF1FPPKPKDTLMISLTPRVTCVVVDVSQDBPBVQFTWFVDNKPV 165
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                                                                                                                                                                                                                                                                                                                    66.3%; Score 889; DB 1; 72.3%; Pred. No. 2.7e-61; tive 24; Mismatches 36
                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #status experimental
                                                                                                                                                                                                                                                                                                                                                                                 Length 329;
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A;Accession: I47158
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: UNIPARC:UPI0000115523; EMBL:U03778; NID:g433121;
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47158
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J. Immunol. 1
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                 197 VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSBFGK 247
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153, 3565-3573, 1994
                                                                                           AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPP
                                                                                                                                                                                                                                             GGDKTHTCPPCPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                          AIGQSREPQVYTLPPPAEELSRSKVTLTCLVIGFYPPDIHVEWKSNGQPEPENTYRTTPP
                                                                                                                                                VDGVEVHTAETRPKEEQFNSTYRVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISK 217
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QQDVDGTFFLYSKLAVDKARWDHGDKFECAVMHEALHNHYTQKSISKTQGK 328
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in: immunoglobulin homology <IMM>
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71.0%;
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1 MIEGPTLRQWLAARAGGGGG.....MHEALHNHYTQKSLSLSPGK 247
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06GMX6 HUMAN
06GNX6 HUMAN
06GNX6 HUMAN
0727P5 HUMAN
0727F5 HUMAN
07275H HUMAN
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7 homo sapien
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OCHEMISTRY 9:3161-3170(1970). [OTEIN SEQUENCE OF 136-329 (EU). IDLINE-71064025; PubMed=5530842; Itishauser U., Cunningham B.A., Bennett C., Konigsberg W.H., lelman G.M.; lelman G.M.; he covalent structure of a human gamma G-immunoglobulin. 8. 1:id sequence of heavy-chain cyanogen bromide fragments H5-H7. ochemistry 9:3171-3181(1970).	LINGUIDE SEQUENCE. DILINES-82274238; PubMed=6287432; Lison J.W., Berson B.J., Hood L.E.; The nuclectide sequence of a human immunoglobulin C gammal gicleic Acids Res. 10:4071-4079(1982). NOTEIN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU). DILINES-71064024; PubMed=5489771; DILINES-71064024; PubM	RESULT 1 IGHG1 HUMAN ID TGHG1 HUMAN STANDARD; PRT; 330 AA. AC P01857; DT 21-UUL-1986 (Rel. 01, Created) DT 21-UUL-1986 (Rel. 01, Last sequence update) DT 10-MAY-2005 (Rel. 47, Last annotation update) DT 10-MAY-2015 (Rel. 47, Last annotation update) DE IG gamma-1 chain C region. GN Name=IGHG1; OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Ho OC Homo. OX NCBI_TaxID=9606;	32 1142 85.2 521 2 QBN4Y9 HUMAN QBn4Y9 1 33 1139.5 85.0 464 2 Q6MZU6_HUMAN Q6mzu6 1 34 1137.5 84.8 465 2 Q6P6C4 HUMAN Q6p6c4 1 35 1135.5 84.7 327 1 IGHG4_HUMAN Q6p6c4 1 36 1135.5 84.7 473 2 QBNFC63_HUMAN Q6p6c4 1 37 1131 84.3 509 2 QBNFT1_HUMAN QBnfL7 1 38 1128.5 84.2 470 2 Q6SCN4_HUMAN Q8nfL7 1 39 1126.5 84.0 476 2 Q6MZX7_HUMAN Q6Bcn4 1 41 917.5 68.4 0 290 1 IGHG3_HUMAN Q6mzx7 1 42 909 67.8 337 2 Q95M34_HORSE
H5-	x , ,	Euteleostomi; arrhini; Hominidae;	Q8n4y9 homo sapien Q6mzu6 homo sapien Q6p6c4 homo sapien Q6p6c4 homo sapien Q8tc63 homo sapien Q8tc63 homo sapien Q8tc1 homo sapien Q68cn4 homo sapien Q6mzx7 homo sapien P01860 homo sapien P01870 oryctolagus Q95m34 equus cabal P01862 cavia porce P20761 rattus norv Q5m839 rattus norv

DISULFIDE BONDS.

gamma

G-immunoglobulin.

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EMBL, J00228, AAC82527.1; ALT_INIT; Genomic_DNA.
R PIR; A9343; GHHU.
R PDB; 1AJY; X-ray; H=1-103.
R PDB; 1AJX; X-ray; H=1-101.
PDB; 1D5B; X-ray; H=1-101.
R PDB; 1D5B; X-ray; H=1-101.
R PDB; 1D5V; X-ray; H=1-101.
R PDB; 1D5V; X-ray; A/B=106-329.
R PDB; 1E4K; X-ray; A/B=106-329.
R PDB; 1FC1; X-ray; A/B=106-329.
R PDB; 1FC2; X-ray; A/B=107-330.
R PDB; 11ZH; X-ray; B/D=1-103.
R PDB; 11ZH; X-ray; B/D=1-103.
R PDB; 11IX; X-ray; B/D=1-103.
R PDB; 11IX; X-ray; B/D=1-103.
R PDB; 11XX; X-ray; A/B=107-330.
R PDB; 12XX; X-ray; A/B=107
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"Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- MISCELLÂNEOUS: Nie has the GlM(17) allotypic marker, 9 GlM(1) markers, 239-D and 241-L. KOL and EU sequences GlM(3) marker and the GlM (non-1) markers.
-!- MISCELLANEOUS: Nie allso differs in the amidation state 116, 198, 269 and 272.
-!- MISCELLANEOUS: EU also differs in the amidation states 155, 166, 177, 195, 198, 269, and 272 and in the order
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
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Biochemistry 9:3188-3196(1970).
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Biochemistry 20:2361-2370(1981).
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D -> E (in G1M(non-1) marker)

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L -> M (in G1M(non-1) marker)
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC073766; AAH73766.1; -; mRNA.

R GO; GO:0016021; C:integral to membrane; IEA.

R InterPro; IPR003599; Ig.

R InterPro; IPR003597; Ig. G1.

R InterPro; IPR003597; Ig. G1.

R InterPro; IPR003597; Ig. MHC.

R InterPro; IPR003006; Ig. MHC.

R InterPro; IPR003596; Ig. W.

R InterPro; IPR003596; Ig. W.

R Pfam; PF07654; C1.set; 3.

R SMART; SM00409; IG; 2.

R SMART; SM00409; IG; 2.

R SMART; SM00406; IGv; 1.

R SMART; SM00406; IGv; 1.

R PROSITE; PS050835; IG LIKE; 4.

R PROSITE; PS050835; IG LIKE; 4.

R PROSITE; PS05099; IG. MHC; UNKNOWN_2.

SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
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RY MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Ahtring M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.M., Schmutz J., Myers R.M.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human roll of the state of 
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Best Local Simi
Matches 227;
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003396; Ig_v.
Pfam; PF07654; C1-set; 3.
                                                                                                                                                                                                Submitted (JUN-2004) to the EMBL; BC072419; AAH72419.1; HSSP; P01861; 1ADQ.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q6IN78;
05-JUL-2004
                                                                                                                                                                                                                                                                                                  TISSUE=Peripheral Nervous System;
NIH MGC Project;
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Name=IGHG1;
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Pred. No. 4.8e-90;
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                                                                                                                                                                                                                                                                                               RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length human and more companies of more than 15,000 full-length human and more companies of more than 15,000 full-length human and more companies of more than 15,000 full-length human and more companies of more than 15,000 full-length human and more companies of more than 15,000 full-length human and more companies of more than 15,000 full-length human and more companies of more than 15,000 full-length human and more companies of more than 15,000 full-length human and more companies of more than 15,000 full-length human and more companies of more than 15,000 full-length human and more companies of more than 15,000 full-length human and more companies of more than 15,000 full-length human and companies of m
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Best Local Similarity 100
Matches 227; Conservative
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10-MAY-2005
10-MAY-2005
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SMART; SHOULDER I IGY; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS60290; IG MHC; UNKNOWN 2.
PROSITE; PS60290; IG MHC; UNKNOWN 2.
PROSITE: PS60290; IG MHC; UNKNOWN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00409;
SMART; SM00407;
SMART; SM00406;
          Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases EMBL; BC092518; AAH92518.1; -; mRNA. SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                           TISSUE=Lymph;
NIH MGC Proje
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606
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                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                     mouse cDNA
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                                                                                                                  Project;
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                                                                                                                                                                                                                                                                                     sequences.";
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RESULT 5
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AC Q7Z7P5 T
AC Q7Z7P5 T
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DT 01-MAR-2
DT 101-MAR-2
DR HOMO SAP
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OC HOMO .

OC HOMO .

ACBI-TAX
RN [1]-TAX
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RN ALISCHAL
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altachul S.F. Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Whilialon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
RA Whiling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
"Generation and initial analysis of more than 15,000 full-length human
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Best Local Similarity
Matches 227; Conser
                               EMBL; BC051328; AAH513
HSSP; P01857; 1HZH.
SMR; Q7Z7P5; 20-469:
InterPro; IPR007110; I
InterPro; IPR003597;
InterPro; IPR003006; I
InterPro; IPR003596; I
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Q1-OCT-2003
Q1-OCT-2003
Q1-MAR-2004
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Mammalia; Eutheria;
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Name=IGHG1;
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                             Submitted (APR-2003)
                                                                                                                                                                                                                                                                         TISSUE=Spleen;
NIH MGC Projec
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                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.
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      C1-set;
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Pred. No. 4.9e-90;
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                                                                                                                                                                  RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rohas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Hitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Warra M.A.,
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",

Danie G. 1600 (2002)
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EMBL; BC053984; AAH539
HSSP; P01857; 1HZH.
InterPro; IPR007110; J
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Q7Z5W1 HUMAN
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Hypothetical protein.
Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini; Hominidae;
                                                                   Strausberg R.;
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01-OCT-2003 (TrEMBLrel.
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                                                                                                                         NUCLEOTIDE SEQUENCE
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PROSITE; PS50835; IG_LIKE;

PROSITE; PS00290; IG_MHC; I
Immunoglobulin domain.
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                                                                                                                                                                  RX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Bischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Green E.J., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Blakesley R.W., Schein J.E., Jones S.J.M., Marra M.A.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
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QGPUJA4 HUMAN PRELIMINARY;
QGPUJA4;
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InterPro; IPR003596; Ig v.
Pfam; PP070554; C1-set; 3.
SMART; SM00406; IGv; 1.
SMOSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_MHC; UNKNOWN 2
PROSITE; PS00290; IG_MHC; UNKNOWN 2
Hypothetical protein; Immunoglobulis
SEQUENCE 470 AA; 51204 MW; 778C
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TISSUE=Primary B-Ce
NIH MGC Project;
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Mammalia; Eutheria; E
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Last sequence update)
Last annotation updat
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Pred. No.
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Best Local S
Matches 227
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InterPro; IPR007110; Ig-11.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003597; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP07654; C1-set; 3.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00299; IG_MHC; UNKNOUSEQUENCE 470 AA; 51716 MW;
                                                            InterPro; IPR003159; Ig. Like. InterPro; IPR00319; Ig_like. InterPro; IPR003597; Ig_c1. InterPro; IPR003597; Ig_MC. InterPro; IPR003596; Ig_W. InterPro; IPR003596; Ig_V. If am; PF07554; C1-set; 3. SMART; SM00409; IG; 2. SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                   The German cDNA Consortium;
Wambutt R., Heubner D., Mewes H.W., Weil B., A
Fobo G., Han M., Wiemann S.;
Fobo G., Han M., Wiemann S.;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ
EMBL; BX640627; CAB45781.1; -; mRNA.
HSSP; P01861; 1ADQ.
                 PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50290; IG_MIC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 472 AA; 51724 MW; 26CB3
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                              TISSUE=Rectum
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                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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Pred. No. 4.9e-90;
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                  26CB340D0046D279 CRC64;
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Best Local (
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QSEFES F
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SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIEE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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InterPro;
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InterPro;
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Anti-RhD monoclonal T125 gammal heavy chain precursor.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases EMBL; AY894992; AAW82028.1; -; mRNA.
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Klein P.,
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                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Pfam; PF07686; V-set; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence determination
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2; IPR003599; Ig.
2; IPR007110; Ig-11ke.
20; IPR003597; Ig_C1.
20; IPR003006; Ig_MHC.
20; IPR003596; Ig_V.
20; IPR003596; Ig_V.
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GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                           GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                                    DKTHTCPPCPAPELLGGPSVPLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
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                                               GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
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Pred. No. 5e-90;
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Pred. No. 4.9e-90;
0; Mismatches 0;
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anti-RhD monoclonal T125
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e recombinant human anti-RhD
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Wefernan K.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA secuences"."
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                                                                                                                 Query Match
Best Local S
Matches 227
                                                                                                                                                                                                                                                                       L Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC073782; AAH73782.1; -; mRNA.

R GO; GG:0016021; C:integral to membrane; IEA.

R InterPro; IPR003599; Ig.

R InterPro; IPR003597; Ig cl.

R InterPro; IPR003597; Ig cl.

R InterPro; IPR003596; Ig w.

R Ffam; PF07654; Cl-set; 3.

R SMART; SM00409; IG; 2.

R SMART; SM00409; IG; 1.

R SMART; SM00406; IGw; 1.

R PROSITE; PS00835; IG LIKE; 4.

R PROSITE; PS00835; IG LIKE; 4.

R PROSITE; PS00290; IG LIKE; 4.

R PROSITE; PS00290; IG LIKE; 4.
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W7_HUMAN
Q6GMW7_F
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Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Ev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse cDNA sequences."
c. Natl. Acad. Sci. U.S
  249
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DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                             DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
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                                                                                                                                                                                                                                475 AA;
                                                                                                                 Conservative
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                                                                                                                                                                                                                             51987 MW;
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                                                                                                                                         91.9%;
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                                                                                                              Score 1233; D; Pred. No. 5e-
0; Mismatches
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Last sequence update)
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Telmerstion And initial analysis of more than 15,000 full-length human
   Query Match
                                                                                                           InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR0031597; Ig-c1:
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_V.
InterPro; IPR003596; Ig_V.
Pfam; PP07554; C1-set; 3.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 3.
SMART; SM00407; IGC1; 3.
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_MHC; UNKNOWN_2
                                                          PROSITE; PS50
PROSITE; PS00
Hypothetical
SEQUENCE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ
EMBL; BC073773; AAH73773.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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476 AA; 5
                                                                 52286 MW;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Factor VII active site mutant immunoconjugate.
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Eukaryota; Metazoa; C
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Submitted (FEB-2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Targeting tissue factor on tumor vascular endothelial cells and cells for immunotherapy in mouse models of prostatic cancer."; Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Q96PQ8; 39-180, 191-444, 447-679.
embl; ENSG00000057593; Homo sapiens.
GO:0005576; C:extracellular region;
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Chordata, Craniata, Verteura
                                                                                                                                                                                                                                                     ; Peptidase_S1A.
; Peptidase_S1_S(
; VitK_dep_GLA.
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EGF_II.

EGF_
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-; mRNA.
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RI Villalon D.K., Muzny D.M., Sodergran R.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergran R.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergran B.J., Dickson M.C.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Holteria D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Formal Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
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SMART; SM000407; IGC1; 1.

SMART; SM000407; IGC1; 1.

SMART; SM00020; Tryp_SBc; 1.

PROSITE; PS00010; ASX HYDROXYL; UNKNOWN 1.

PROSITE; PS00010; ASX HYDROXYL; UNKNOWN 1.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS00011; GLA 1; UNKNOWN 1.

PROSITE; PS00015; IG LIKE; 2.

PROSITE; PS00187; IG MC; UNKNOWN 1.

PROSITE; PS00290; IG MC; UNKNOWN 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN SER; 1.

PROSITE; PS00134; TRYPSIN SER; 1.

PROSITE; PS00135; TECET MC; UNKNOWN 1.
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Best Local :
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Eukaryota; Metazoa; Cho.
Mammalia; Eutheria.
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05-JUL-2004
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(TrEMBLrel.
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100.0%;
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Pred. No. 7.9e-90;
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572 140

632 200 80

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Acted the same of the

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INTERPRO; IPRO07110; IG-like.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG_C1.

DR InterPro; IPR003596; IG_MHC.

DR InterPro; IPR003596; IG_V.

DR Pfam; PF07654; C1-set; 3.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGC1; 3.

DR SMART; SM00407; IGC1; 1.

PR PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS50290; IG_MHC; UNKNOWN_2.

1 Hypothetical protein.

SEQUENCE 473 AA; 5124.
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Best Local S
Matches 226
Submitted (JAN-2005) to the EM

BMBL; BX640947; CAE45972.1; -;

HSSP; P01861; 1ADQ.

SMR; Q6MZQ6; 20-475.

InterPro; IPR003599; Ig.

InterPro; IPR003199; Ig-like.

InterPro; IPR003197; Ig-C1.

InterPro; IPR003197; Ig-C1.

InterPro; IPR003197; Ig-C1.

InterPro; IPR003196; Ig_WHC.
                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation updat
Hypothetical protein DKFZp686G11190.
Name=DKFZp686G11190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                         The German cDNA Consortium;
Bahr A., Lauber J., Mewes H.W., Weil B.,
Han M., Wiemann S.;
                                                                                                                                           TISSUE=Esophagus tumor;
                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                     Q6MZQ6;
Q6MZQ6;
                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                        DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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l. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nervous
                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.6%;
99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          System;
                                                                                    EMBL/GenBank/DDBJ
-; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ
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Pred. No. 1
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DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD

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RESULT 15
Q6N094 HUMAN
ID Q6N094 H
AC Q6N094 H
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DF O5-JUL-2
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Matches 226
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig c1.
InterPro; IPR003596; Ig_MCC.
InterPro; IPR003596; Ig_V.
Pfam; PP07654; C1-set; 3.
SMART; SM00409; IG; 2.
SMART; SM00409; IG; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS00290; IG_MC; UNKNO
Hypothetical protein.
SEQUENCE 480 AA; 52612 MM;
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SMART; SM00409; IG; 2.
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SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4
PROSITE; PS50835; IG_MHC; UN
Hypothetical protein.
SEQUENCE 475 AA; 52043 MW
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Q6N094;
Q6N094;
Q6N094;
Q5-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686001196.
Namme=DKFZp686001196;
Namme=DKFZp686001196;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homin
                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Bsophagus tumor;
The German cDNA Consortium;
Wambutt R., Heubner D., Mewes H.W.,
Pobo G., Han M., Wiemann S.;
Submitted (JAN-2005) to the EMBL/Ger
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BX640622; CAE45776.1; HSSP; P01861; 1ADQ.
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Score 1229; DB 2;
Pred. No. 1.1e-89;
0; Mismatches 1;
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Search completed: April 4, 2006, 13:15:13 Job time : 190.806 secs	434 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 480	DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 247	374 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 433	141 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 200	314 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 373	81 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 140	254 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 313

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Aab17253	Aab17255	Aab17251	Aab17254	Aar93356	Aar93348	Aar93345	Aar93377	Aar93346	Aar93344	Aar93343	Aar93363	Aar93362	Aar93360	Aar93365	Aar93364	Aar93379	Aar93349	Aar93353	Aar93359	Aar93352	
EES	SH3	SH3	SH3	FYN	SRC	SRC	Grb	SRC	SRC	SRC	LYN	LY.	NA7	LYN	NAT	Grb	FYN	FYN	NAT	RYN	
antag	antag	antag	antag	d NAT	prote	prote	Grb-2 pro	d NAT	prot	prote	prote	/PI3K	prote	prote	prote		prote	prote	prote	prote	

ALIGNMENTS

RESULT 1
AAWII128
AIF JAWII 128
AC AAWI
XX AXX
DI Src
XX Src;
XX Src; 22-JUL-1994; 07-JUN-1995; Src; SH3; Src homology region 3; binding affinity; oncogenic protein tyrosine kinase; signal transduction; RNA processing, Sparks AB, 24-JUL-1995; 08-FEB-1996. WO9603649-A1 Synthetic. trafficking; 27-JUN-1997 AAW11128; AAW11128 standard; peptide; 7 AA. (UYNC-) UNIV NORTH CAROLINA SH3 domain-binding Kay BK, (first entry) translation 94US-00278865. 95US-00483555. 95WO-US009382 Thorn JM, peptide preferred Quilliam LA, core Der sequence protein;

Peptide with binding affinity for Src homology region 3 (SH3) domains proteins - useful for e.g. modulating signal transduction pathways at cellular level, esp. protein tyrosine kinase-mediated. the

WPI;

Disclosure; Page 62; 116pp; English.

AAW11128 represents a preferred core sequence of a set of peptides that bind to the Src SH3 domain. The SH3 binding peptides are useful in modulating signal transduction pathways at the cellular level (especially protein tyrosine kinase-mediated), modulating oncogenic protein activity, or providing compounds for the development of drugs with the ability to modulate broad classes, as well as specific classes, of proteins involved in signal transduction and also for regulating the processing, translation of RNA. Conjugates of the peptides with detectable labels or imaging agents are useful for imaging cells, tissues and organs in which Src or Src-related proteins are expressed

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RRESULT 2
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                                                                                                                                                                                                                                                                         AAW17010 is the consensus sequence of a set of SRC SH3-binding peptides derived from a biased peptide library, exhibiting selective SH3 binding. SH3 binding peptides are useful in modulating signal transduction pathways at the cellular level (especially protein tyrosine kinase-mediated), modulating oncogenic protein activity, or providing compounds for the development of drugs with the ability to modulate broad classes, as well as specific classes, of proteins involved in signal transduction and also for regulating the processing, trafficking or translation of RNA. Conjugates of the peptides with detectable labels or imaging agents are useful for imaging cells, tissues and organs in which Src or Src-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
protein tyrosine kinase; signal transduction; RNA processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide with binding affinity for Src proteins - useful for e.g. modulating cellular level, esp. protein tyrosine
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07-JUN-1995;
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95US-00483555.
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Pred. No. 2e+
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Pred. No. 2e+06;
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RESULT 3

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RESULT 4
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Matches
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Rider JE;
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Unidentified
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                                          AAW79781 standard; peptide; 7
                                                                                                                                                                                                                                             Sequence 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  certain lymphokine(s), e.g. interleukin-1.
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llarity 100.0%;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method and apparatus for performing an cleatrochemical assay for detecting specific binding between members of a biological binding pair. The apparatus detects specific binding between a first member immobilised on an electrode and a second member which is biologically labelled, in the presence of an electrochemical mediator. The method may be used for performing binding and competitive binding assays. It may be used in performing high throughput screening assays for detecting inhibition of specific binding between the members of the binding pair for use in drug development, biochemical analyses and protein purification assays. The present sequence is an example of a peptide which is used in labelled form as a second binding member in the above assay. The peptide acts as a surrogate ligand for the the first member. Specifically, the peptide is a proline-rich peptide which binds with Src SH3 domain
                   autoimmune disease; cytostatic; antiasthmatic; thrombolytic; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNP; antaginhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                               Src antagonist
                                                                                                                                                     Modified peptide; therapeutic agent; fusion;
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16-SEP-1997;
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analysis; purification; proline-rich; Src SH3.
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97US-0059049P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                               ID NO:323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Src
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                          Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                               factor;
                                                                                                                                                          cancer
                                                                                                   antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                               VEGF ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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in the
                                                                                                      MMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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AAB17

AAB17226 standard;

peptide;

밁 S

thrombosis;

dothelial growth factor; pharmaceutical.

Modified peptide; therapeutic agent; fusion; Pc domain; cancer; autoimmune disease; cycostatic; antiasthmatic; thrombolytic; VEGP; immunosuppressive; EPO; TPO; CTLA; mimetic; II-1; TNF; antagonist; Moinhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma;

SH3 antagonist peptide sequence SEQ ID NO:282.

31-OCT-2000 AAB17226;

(first entry)

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RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes composition of matter (I) comprising an CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is: CC (XI)a-FI-(XZ)b, where: FI = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L1)c-P2-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3
                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                               Best
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39; Page 308; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         composition of matter comprising an Fc domain and pharmacologically e peptides, useful for treating cancer and autoimmune diseases.
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                                                                                                                                                          1 RPLPPLP 7
                                                                                                                                                                                                                                                 Similarity 7; Conserv
                                                                                                         RPLPPLP
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                                                                                                                                                                                                                                                         Conservative
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99US-00428082
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                                                                                                                                                                                                                                                     <u>,</u>
                                                                                                                                                                                                                                                     Score 41; DB
Pred. No. 2e+
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
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                                                                                                                                                                                                                                                                                           2e+06;
                                                                                                                                                                                                                                                                                                                                 DB
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RESULT 7
AAY69979
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p3, and p4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombostis, or autoimmune diseases. The use of an PC domain (rather than a Pab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes composition of matter (1) comprising Fc domain, pharmacologically active peptides, and linkers. Where (1) (X1)a-F1-(X2)b, where: F1 = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, (L2)d-P2-(L3)e-P3-(L4)f-P4 where P1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pha
active peptides, useful for treating cancer and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAY-2000
                                                                                                                                  Electrochemically labelled peptide; probe; electrochemical assay; binding detection; biological binding pair; electrochemical analydrug detection; drug development; biochemical analysis; Src; protein purification assay; SH3 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 39; Page 295; 608pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-1999;
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                                                                                                                                                                                                                                               14-APR-2000
                                                                                                                                                                                                                                                                                                          AAY69979 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7
               28-MAY-1999;
                                                                           WO9964847-A1
                                                                                                         Synthetic
                                                                                                                                                                                                                 Src SH3 region binding peptide #1.
                                            16-DEC-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                1 RPLPPLP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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99US-00428082.
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               99WO-US011848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 3;
Pred. No. 2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                i,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an Fc domain and pharmacologically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases
                                                                                                                                                                    analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is:
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RESULT 8
AAB50762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents an Src SH3 region binding peptide. The invention cc relates to an apparatus for performing an electrochemical assay for cdetecting binding between members of a biological binding pair. The apparatus has: a first electrode (comprising a conducting or conducting surface); a second, reference electrode (comprising a conducting metal in contact with an aqueous electrolyte solution); and a cc third, auxiliary electrode; where each electrode is connected to a cc potentiostat and is in contact with an electrolyte solution containing both members of a biological binding pair. The second member of the cc binding pair is electrochemically labeled with a chemical species capable of participating in a reduction/oxidation reaction at the surface of the cfirst electrode under conditions where an electrical potential is applied to the electrical potential is applied to the apparatus when an cc electrical potential is applied to the electrodes, and the current is reduced upon binding of the second member of the biological binding pair to the first member of the pair. The method can be used for to the first member of the pair. The method can be used for conditions a means for rapid, high throughput screening of biologically active
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apparatus for electrochemical analyses for drug detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-136855/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  We1ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUN-1998;
                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                   PDE4D5; cAMP-specific phosphodiesterase; RACK1; modulator; receptor for activated C-kinase.
                                                                                                                                                                                                                                                                                                Human cAMP-specific phosphodiesterase PDE4D5 modulator SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                          AAB50762 standard; peptide; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (XANT-) XANTHON
            WPI; 2001-061280/07
                                       Bolger GB, Houslay MD,
                                                                                                                                                                30-NOV-2000
                                                                                                                                                                                            WO200071080-A2
                                                                                                                                                                                                                                                                                                                                20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                             AAB50762;
                                                                                                    20-MAY-1999;
                                                                                                                               20-MAY-2000; 2000WO-US013961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RPLPPLP 7
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| RPLPPLP
                                                                      UNIV UTAH RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                    99US-0135035P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 41; DB 3; Length 7; 100.0%; Pred. No. 2e+06;
                                          Steele MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 °.
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                                          Yarwood
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The present invention describes a vehicle-peptide molecule (I) or its multimers. (I) can have antiinflammatory, antitumour, immunosuppressive, cytostatic, antitheumatic, antiarthritic, antidiabetic, ophthalmological, antidanaemic, anorectic, antiinfertility, haemostatic, dermatological and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNF-alpha inhibitor; interleukin 1 antagonist; TL-1 antagonist; TMP; TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmologicantianaemic; anorectic; antiinfertility; haemostatic; dermatological; neuroprotective; inflammatory disease; autoimmune disease; tumour groy cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obessleep disorder; neurological degenerative disease; anaemia; thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides methods and peptides for use in identifying modulators of the cAMP-specific phosphodiesterase isoform PDE4D5. These act by modulating the interaction of PDE4D5 with the receptor for activated C-kinase (RACKI). The modulators are useful in treatment of various conditions
                                                                                                                                                                                                                         Novel vehicle-peptide molecule or its inflammatory and autoimmune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening drugs that modulate activity of cAMP-specific phosphodiesterase for treating various conditions by detecting modulation of interaction between phosphodiesterase and activated C-kinase receptor by the drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-2000; 2000US-00563286
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                                                                                                                                                                                                                                                                                                                                                                Liu C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SH3) antagonist peptide SEQ ID NO:282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                      Cheetham JC,
                                                                                                                                       176pp;
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                                                                                                                                                                                               obesity,
                                                                                                                                          English
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Pred. No. 2e+06;
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                                                                                                                                                                                               or its multimers useful for treating seases, cancer, rheumatoid arthritis, sleep disorders and infertility.
                                                                                                                                                                                                                                                                                                                                                                      Boone
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                                                                                                                                                                                                                                                                                                                                                                      JC,
                                                                                                                                                                                                                                                                                                                                                                      Gudas JM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best
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                                                                                                                                                                                                                                                                                                                                              erythropoletin; TPO; tumour necrosis factor alpha inhibitor; TWP; TWP-alpha inhibitor; interleukin 1 antagonist; TWP; antagonist; TWP; TPO mimetic peptide; EMP; VEGF antagonist; TMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological antianaemic; anorectic; antiinfertility; haemostatic; dermatological; neuroprotective; inflammatory disease; autoimmune disease; tumour grocancer; rheumatoid arthritis; diabetic retinopathy; infertility; obes sleep disorder; neurological degenerative disease; anaemia;
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                                                                                                                                                                                                                                                          WO200183525-A2
                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified peptide;
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                                                                                                                                                                                                                                                                                                                                   thrombocytopaenia; metastatic
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                                                                                                                                    AMGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPLPPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmacologically active peptide SEQ ID NO:323
                                                                                                      Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                      Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mimetic; Fc domain;
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Pred. No. 2e+
0; Mismatches
                                                                                                                                                                                                                                                                                                                                  tumour; systemic
                                                                                                      Boone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fusion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IgG;
                                                                                                                                                                                                                                                                                                                                                                r growth; obesity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Low
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Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.

Claim 39; Page 61; 176pp; English

invention describes a vehicle-peptide molecule (I) or its

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RESULT 11
ADJ73499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7
New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region, useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003084477-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mimetic; CDR min
cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exemplary mimetic
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                                                                                                                                                                                      WPI; 2003-804237/75
                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-2002; 2002US-0368791P
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                                                                                                                                                                                                                                                                                                                                (CENZ ) CENTOCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunomodulator;
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                                                                                                                                                                                                                                                             g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDR mimetibody; gene therapy; transgenic; immune; scular; infectious; malignant; neurologic disease; anaemia; dulator; cardiant; antimicrobial; cytostatic; neuroprotective.
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                                                                                                                                                                                                                                                         Knight DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide
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                                                                                                                                                                                                                                                             Scallon BJ,
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Pred. No. 2e+
0; Mismatches
                                                                                                                                                                                                                                                             Ghrayeb
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                                                                                                                                                                                   New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region, useful for preparing a composition for treating e.g., immune,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mimetic; CDR mimetibody; gene therapy; transgenic; immune;
cardiovascular; infectious; malignant; neurologic disease; anaemia;
immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
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portions or variants thereof. Specifically, it refers to an antibody fragment where a protein has been inserted into, or replaces a portion of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which itself comprises at least one human framework region and at least one ligand binding region (LBR). The present invention describes human
                                                                                                                                                                                                                                                           WPI; 2003-804237/75
                                                                                                                                                                                                                                                                                             Heavner GA,
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                                                                                                       This
                                                                                                                                       Disclosure; SEQ ID
                                                                                                                                                                          cardiovascular or neurologic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2003
                                                                                                                                                                                                                                                                                                                              (CENZ )
                                                                                  invention relates to novel mammalian CDR mimetibodies, specific on or variants thereof. Specifically, it refers to an antibody
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7; Conservative
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                                                                                                                                                                                                                                                                                             Knight DM,
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                                                                                                                                         827; 97pp; English.
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Pred. No.
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                                                                                                                                                                             This invention relates to CH1 deleted mimetibodies (and the DNA second them), compositions, methods and uses. The invention ruseful for the development of compounds with an immunosuppressive, cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, antibacterial, virucide or fungicide activity. In addition, the discondination of the discond
antibacterial, virucide or fungicide activity. In addition, the discloss sequences may prove useful for gene therapy. The CH1-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell, tissue, organ or animal, specifically for modulating, treating, alleviating, preventing the incidence or reducing the symptoms of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New CH1-deleted mimetibody polypeptides and nucleic acids, useful modulating, treating, alleviating, preventing an immune, cardiovas or neurodegenerative disease or disorder, anemia, cancer, or infec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant; hypotensive; neuroprotective; nootropic; antibacterial; virucide; fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hypertension; heart failure; neurodespenerative; multiple sclerosis; dementia; Alzheimer's disease; anaemia; cancerous condition; infectious disease; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preparing compositions for modulating, treating or reducing the symptoms of immune, cardiovascular, infectious, malignant and/or neurologic diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, cardiant, antimicrobial, cytostatic and neuroprotective activities. This peptide sequence is an SH3 antagonist peptide sequence used to make a mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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KA,
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100.0%; Pr
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This invention relates to CH1 deleted mimetibodies (and the DNA sequences which encode them), compositions, methods and uses. The invention may be useful for the development of compounds with an immunosuppressive, cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, antibacterial, virucide or fungicide activity. In addition, the disclosed sequences may prove useful for gene therapy. The CH1-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell, tissue, organ or animal, specifically for modulating, treating, alleviating, preventing the incidence or reducing the symptoms of an immune, cardiovascular (for example arrhythmia, hypertension or heart failure), or neurodegenerative (for example multiple sclerosis, dementia or Alzheimer's disease) diseases or disorders, anaemia, cancerous
                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                      New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovasculor neurodegenerative disease or disorder, anemia, cancer, or infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fungicide; gene therapy; immune disorder; cardiovascular di
arrhythmia; hypertension; heart failure; neurodegenerative;
multiple sclerosis; dementia; Alzheimer's disease; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or Alzheimer's disease) diseases or disorders, anaemia, cancerous conditions, or infectious diseases (for example bacterial, viral cfungal infection). The present sequence is that of a peptide which used during the creation of a mimetibody of the invention.
                                                                                                                                                                                                          Claim 3;
                                                                                                                                                                                                                                                    modulating, treating, allevider or neurodegenerative disease
                                                                                                                                                                                                                                                                                                                                                     Kutoloski
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                                                                                                                                                                                                          ID NO 955;
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                                                                                                                                                                                                      129pp; English.
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                                                                                                                                                                                                                                                      cardiovascular, or infectious
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W CH1 deleted mimetibody; osteopathic; cardiovascular-Gen; whereatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; wy gynaecological-Gen; hepatotropic; haemostatic; immunomodulator; whilallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic; wo phthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor; where the some disorder; joint disorder; cardiovascular disorder; whental disorder; oral disorder; dermatological disorder; ear disorder; whose disorder; throat disorder; endocrine disorder; metabolic disorder; whose disorder; throat disorder; endocrine disorder; metabolic disorder; whose disorder; haematological disorder; immunological disorder; was allergic disorder; haematologic disorder; musculoskeletal disorder; woncological disorder; neurological disorder; nutritional disorder; wophthalmologic disorder; pediatric disorder; psychiatric disorder; pulmonary disorder; psychiatric disorder; wrenal disorder; pulmonary disorder.
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                                                                                                                                                                                          New CH1 deleted mimetibody polypeptide and nucleic acid, useful for diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CH1 deleted mimetibody-related peptide SeqID827.
                                                                                                                                                                                                                                                                                                                                                                                       28-JUN-2002; 2002US-0392431P.
19-SEP-2002; 2002US-0412144P.
                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2003; 2003WO-US020495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
This invention relates to CH1 deleted mimetibodies (and the DNA sequences which encode them), compositions, methods and uses. The invention may be useful for the development of compounds with an osteopathic, cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen, gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic, immunomodulator, antiallergic, muscular-Gen, cytostatic, antiinflammatory, neuroleptic, ophthalmological, nephrotropic or
                                                                                                                                          Claim 15;
                                                                                                                                                                           nutritional
                                                                                                                                                                                                                                                                  WPI; 2004-082872/08
                                                                                                                                                                                                                                                                                                                      Heavner GA,
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                                                                                                                                                                                                                                                                                                   Kutoloski KA;
                                                                                                                                                                                                                                                                                                                                                        (CENZ ) CENTOCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
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                                                                                                                                                                                                                            Sequence 7 AA;
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ALIGNMENTS

C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #text_change 09-Jul-2004
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7509; PC7101
R;Ezumi, Y: Uchiyama, T:; Takayama, H.
Blochem. Biophys. Res. Commun. 277, 27-36, 2000
Biochem. Biophys. Res. Commun. 277, 27-36, 2000
A;Title: Molecular cloning, genomic structure, chromosomal localization, and alternati
A;Reference number: JC7509; MUID:20483673; PMID:11027634
A;Contents: Placelet

glycoprotein VI-1 - human
C; Species: Homo sapiens ()

A;Accession: JC7509 A;Molecule type: mRNA A;Residues: 1-339 <EZU>

A;Cross-references: UNIPROT:Q9UIF2; UNIPARC:UPI000006F4A8; DDBJ:AB043819 A;Accession: PC7101

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gene 33 protein, hepatic - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-190 #sequence revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: $03116; $03402; $30568; $08283
R;Chrapkiewicz, N.B.; Davis, C.M.; Chu, D.T.W.; Caldwell, C.M.; Granner, D.K.
Nucleic Acids Res. 17, 6651-6667, 1989
A;Title: Rat gene 33: analysis of its structure, messenger RNA and basal promoter
A;Reference number: $03116; MUID:89385990; PMID:2780291
A;Accession: $03116
A;Molecule type: DNA
A;Residues: 1-459 < CHR>
A;Residues: 1-459 < CHR>
A;Residues: 1-459 < CHR>
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A;Residues: 28-41;62-79;114-142 <EZZ>
A;Residues: 28-61;62-79;114-142 <EZZ>
A;Cross-references: UNIPARC:UPIO00017A509; UNIPARC:UPIO00017A50A; UNIPARC:UPIO00017A50
C;Comment: This protein, which belongs to the immunoglobulin superfamily, is the major or gamma chain as a signal transducing subunit, and plays some roles in cancer cells.
A;Cross-references: UNIPROT:P05432; UNIPARC:UPI000012F0FD; EMBL:X07266; NID:g57568; R;Lee, K.L.; Makkinje, A.; Ch'ang, L.Y.; Kenney, F.T. Arch. Biochem. Biophys. 269, 106-113, 1989
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A;Introns: 62/1; 95/1; 353/1; 638/1; 692/1; 752/1;
C;Keywords: glycoprotein; immunoglobulin; platelet
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A;Title: Molecular cloning and analysis of full-length cDNAs cognate to a rat gene unde A;Reference number: S03402; MUID:89133523; PMID:2916834
A;Recession: S03402
A;Molecule type: mRNA
A;Residues: 1-459 < LBE>
A;Coss-references: UNIPARC:UPI000012F0FD
A;Coss-references: UNIPARC:UPI000012F0FD
A;Note: the authors translated the codon GGA for residue 18 as Lys, TAC for residues 19
A;Note: the authors translated with conceptual translation
A;Accession: B30568
A;Statue: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-17, 'K',19-66,143-191,'T',193-301,'L',303-310,'L',312-395,'L',397-409,'L',
A;Residues: 1-17, 'K',19-66,143-191,'T',193-301,'L';Renney, F.T.
A;Lee, K.L: Makkinje, A.; Ch'ang, L.Y.; Kenney, F.T.
A;Chespers number: S08283
A. Deference number: S08283
J. Biol. Chem. 268, 6839-6842, 1993

A,Title: Alternative splicing gives rise to a nuclear protein tyrosine phosphatase A;Reference number: A46101; MUID:93216607; PMID:8463208

A;Accession: A46101

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-535 <MCL>
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A;Reference number: 224136
A;Accession: T46917
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-477 <AAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein DKPZp762K137.1 - human (fragment) C;Species: Homo sapiens (man) C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_cC;Accession: T46917 R;Ottenwaelder, B.; Mewes, H.W.; Weil, B.; R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Weil, B.;
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                                                                                                                                                                                                                       protein-tyrosine-phosphatase (EC 3.1.3.48) nonreceptor type C;Species: Drosophila melanogaster C;Date: 08-May-1995 #sequence_revision 12-May-1995 #text_cha
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Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ypothetical protein DKFZp762Kl37.1 - human (fragment)
;Species: Homo sapiens (man)
;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                     Accession: A46101
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                                      A;Cross-references: UNIPROT:P22460; UNIPARC:UPI000016AE76; GB:M55513; NID:g189653; P1 R;Philipson, L.H.; Hice, R.E.; Schaefer, K.; LaMendola, J.; Bell, G.I.; Nelson, D.J.; Proc. Natl. Acad. Sci. U.S.A. 88, 53-57, 1991

A;Title: Sequence and functional expression in Xenopus occytes of a human insulinoma A;Title: Sequence and functional expression in Xenopus occytes of a human insulinoma A;Reference number: A38556; MUID:91095456; PMID:1986382
                                                                                                                                                              A; Accession: A56031
A; Molecule type: mRNA
A; Residues: 1-613 < PHI>
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                    A38556
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A;Cross-references: UNIPROT:Q9W0G1; UNIPARC:UPI000016BD13; GB:L11251; NID:g290265; PIDN A;Note: authors translated the codon TTC for residue 382 as Ile, and CGA for residue 52 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type PTP61F; pi C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester l F;60-285/Domain: protein-tyrosine-phosphatase homology <PTP> F;60-285/Domain: protein-tyrosine-phosphatase homology <PTP> F;237/Active site: Cys (phosphocysteine intermediate) #status predicted
                                                                                                                                              C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type PTP61F; protein-tyrosine-C;Keywords: alternative splicing; phosphortein; phosphoric monoester hydrolase; tyros F;60-285/Domain: protein-tyrosine-phosphatase homology cPTPs F;237/Active site: Cys (phosphocysteine intermediate) #status predicted F;237/Binding site: substrate phosphate (Arg) #status predicted
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A;Title: Alternative splicing gives rise to a nuclear protein tyrosine phosphatase A;Reference number: A46101; MUID:93216607; PMID:8463208
A;Accession: B46101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type PTP61F, long splice C;Species: Drosophila melanogaster C;Date: 08-May-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
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A;Note: authors translated the codon TTC for residue 382 as Ile
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A; Residues: 1-548 < MCL>
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Chem. 268, 6839-6842, 1993
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Pred. No. 52;
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potassium channel HK2; potassium channel PCN1; shaker-related

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A;Accession: A00653
A;Accession: A00653
A;Accession: A00653
A;Molecule type: DNA
A;Residues: 1-63 <ANAH>
A;Residues: 1-63 <ANAH>
A;Residues: 1-63 <ANAH>
A;Residues: This color that the codon GAT for residue 14 as Glu
C;Comment: This protein is synthesized as a gag-fgr polyprotein.
C;Cene: Ggr
C;Comment: This protein is synthesized as a gag-fgr polyprotein.
C;Cene: Ggr
C;Superfamily: feline sarcoma virus protein-tyrosine kinase fgr; protein;
C;Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotra
F;1-118/Region: gag polyprotein similarity
F;141-269/Region: actin similarity
F;285-382/Domain: SH2 homology <SH2>
E:400-460/Tomain: SH2 homology <KTN>
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                                                                                                                F;402-660/Domain: protein kinase homology «KIN» F;410-418/Region: protein kinase ATP-binding mol F;432/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Naharro, G.; Robbins, K.C.; Reddy, E.P. Science 223, 63-66, 1984
A;Title: Gene product of v-fgr onc: hybrid A;Reference number: A00653; MUID:84097512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: host Felis sp. (cat)
C;Date: 27-Nov-1985 #sequence revision 26-May-1995
C;Accession: A00653; A03937
R;Naharro, G.; Robbins, K.C.; Reddy, B.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein-tyrosine kinase (EC 2.7.1.112) fgr - C;Species: feline marronm ......
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A;Map position: 12p13.33-12p13.31
C;Superfamily: potassium channel protein drkl
C;Keywords: 9lycoprotein; phosphoprotein; potassium channel; transmembrane protein; vol.
F;125,190/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;557/Binding site: phosphate (Ser) (covalent) #status predicted
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A;Residues: 1-137,'L',139-153,'R',155-213,'R',215-227,'P',229-281,'V',283-578,'QLPPREV'
A;Cross-references: UNIPARC:UPI000016AEEA; GB:M83254; NID:g190202; PIDN:AAA60146.1; PID
A;Experimental source: heart
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Genomics 12, 729-737, 1992
A;Title: Molecular cloning, characterization, and genomic localization
A;Reference number: A38074; MUID:92241872; PMID:1349297
A;Accession: A38074
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A;Residues: 1-54,56-137,'L',139-186,'G',189-213,'R',215-227,'P',229-297,'PTQRGH',309-558
A;Cross-references: UNIPARC:UPI00001779F4; GB:M60451
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A;Molecule type: DNA
A;Rosidues: 1-56,'G',58-137,'L',139-213,'R',215-227,'P',229-545,'QG',546-613 <PH2>
A;Cross-references: UNIPARC: UPI00001779F3; GB.M55513
R;Tamkun, M.M.; Knoth, K.M.; Walbridge, J.A.; Kroemer, H.; Roden, D.M.; Glover, D.P.
FASEB J. 5, 331-337, 1991
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A;Title: Molecular cloning and characterization of two voltage-gated K(+) channel cDNAs

A;Reference number: A39922; MUID:91160866; PMID:2001794
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P; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; pol:
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hypothetical protein YNL152w - yeast (Saccharomyces N;Alternate names: hypothetical protein N1765 C;Species: Saccharomyces cerevisiae C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #C;Accession: S60975; S63104; S63822 R;Nasr, F.; Becam, A.M.; Herbert, C.J. submitted to the EMBL Data Library, October 1995
                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: Clone C16D6 C;Genetics:
                                                                                                                              RESULT
S60975
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A;Map position: X
A;Introns: 42/1
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84870
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F84870
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C;Species: Caenorhabditis elegans
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A; Residues: 1-894 < STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein At2943800 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                           Conservative
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Pred. No.
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A; Map po
A; Note:
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C49507
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Yeast 12, 169-175, 1996
A;Title: The sequence of 36.8 kb from the left arm of chromosome dystrophy kinase.
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A;Experimental source: strain S288C
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potassium channel Kv1.5 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995
C;Accession: A49507; B49507
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A;Map position: 14L
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                                                                                                                                                                                                                                                                                                                     C;Superfamily: potassium channel protein
C;Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPARC:UPI00001779F5; GB:L22218 C;Superfamily: potassium channel protein drk1
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A; Residues: 1-514 < ATT>
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Best Local S
Matches 6
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Residues: 1-409 <NAS>
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RPLPPMP 71
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85.7%;
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                                                                                                                                                                                                                                            Score 39; DB Pred. No. 96; 1; Mismatches
                                                                                                                                                                                                                                            1;
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Pred. No. 76;
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                        #text_change 09-Jul-2004
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conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: C75539
R;White, O; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dc, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodu
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: C75539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Attali, B.; Lesage, F.; Zillani, P.; Guillemare, E.; Honore, E. J. Biol. Chem. 268, 24283-24289, 1993
A;Title: Multiple mRNA isoforms encoding the mouse cardiac Kv1-5 A;Reference number: A49507; MUID:94043264; PMID:8226976
A;Accession: A49507
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A; Accession: B49507
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A;Molecule type: mRNA
A;Residues: 1-602 <ATT>
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A; Residues: 201-602 < AT2>
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A;Experimental source: strain R1
                                                                                                                                                                                                                                                             A;Residues: 1-222 <WHI>
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Best Local
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Best Local
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201 RPVPPLP 207
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                                   1 RPLPPLP 7
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85.7%;
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85.7%;
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                                                                             Score 38; DB
Pred. No. 56;
1; Mismatches
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Pred. No. 1.1e+02;
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T.; Zalewski,
                                                                                 Gaps
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protein-tyrosine kinase (EC 2.7.1.112) TXK - human (;Species: Homo sapiens (man) (species: Homo sapiens (man) (;Species: Homo sapiens (man) (;Species: Homo sapiens (man) (species: Homo sapiens (man) (species: Homo sapiens (man) (species: Lordon sap

sequence identi

(EC 2.7.1.112) TXK - human

I84483

A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-527 <HAR1>

Cross-references:

UNIPROT: P42681; UNIPARC: UPI0000137828;

GB:L27071; NID:g951045;

PID

from GB/EMBL/DDBJ

A; Accession: I84483

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A;Cross-references: UNIPARC:UPI0000028034; GB:L35268; NID:g623442; PIDN:AAA67039.1; PID: A;Note: in Genbank entry MUSRLK, release 116.0, the source is designated as Mus cookii C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology (;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase P;99-137/Domain: SH2 homology <SH3> F;150-246/Domain: SH2 homology <SH3> F;269-527/Domain: protein kinase homology <KIN> F;277-285/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P42682; UNIPARC:UPI0000028034; EMBL:U16145; NID:g562124; PII R;Hu, Q.; Davidson, D.; Schwartzberg, P.L.; Macchiarini, F.; Lenardo, M.J.; Bluestone, J. Biol. Chem. 270, 1928-1934, 1995
A;Title: Identification of rlk, a novel protein tyrosine kinase with predominant express A;Reference number: A55631; MUID:95130578; PMID:7829530
A;Accession: A55631
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I49133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: I4913; A55631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: Tyrosine-protein kinase, proto-oncogene C;Keywords: ATP; phosphotransferase; tyrosine-specific F;89-137/Domain: SH3 homology <SH3>
                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-527 < HUA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mamm. Genome 6, 476-480, 1995
A;Title: The murine form of TXK, a novel TEC kinase expressed in thymus maps to chromos
A;Reference number: I49133; MUID:96059536; PMID:7579892
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A;Map position: 4p12-4p12
A;Introns: 262/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein-tyrosine kinase (EC 2.7.1.112) txk - mouse
N;Alternate names: resting lymphocyte protein-tyro;
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A;Residues: 238-275,'X',277-318 <HAR5>
A;Cross-references: UNIDARC:UPI000011DDEE;
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A;Accession: I38375
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A;Residues: 195-236 <HAR4>
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A;Residues: 128-148 <HAR3>
A;Cross-references: UNIPARC:UPI0000000530; EMBL:U07792;
A;Accession: 138374
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A;Molecule type: DNA
A;Residues: 7-24 <HAR2>
A;Cross-references: UNIPARC:UPI000000052F; EMBL:U07791; NID:g508216; PIDN:AAA19597.1;
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85.7%;
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Pred. No. 1.4e+02;
1; Mismatches 0
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Q80WJ0_MOUSE
Q60908_RHOPA
Q9UIF2_HUMAN
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Q5YME9_NOCFA
Q6PA5_XENLA
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Q6PA5_KENLA
Q8IR4_DROWA
Q8IR4_DROWA
Q8IR4_DROWA
MIG6_RAT
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Q9NSQ8_HUMAN
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NCBI_TaxID=188763;
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Alcendor D.J., McGeoch D.J., Hayward G.S.;
"The human cytomegalovirus genome revisited: comparison with a cytomegalovirus genome.";
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J. Gen. Virol. 84:17-28(2003).
EMBL; AF480884; AAM00667.1; -; Genomic DNA.
SEQUENCE 101 AA; 11945 MW; 3665065T1C6EA442
                                                                                                                                        Bukaryota; Viridiplantae; Streptophyta; En Sparmatophyta; Magnoliophyta; Liliopsida; Ehrhartoideae; Oryzeae; Oryza.
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Nature 414:450-453(2001).
EMBL; AL590451; CAD27048 1; -; Genomic_DNA.
Complete proteome; Hypothetical protein.
SEQUENCE 128 AA; 14388 MW; 9096523574791EFC
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MEDLINB=21576510; PubMed=11719806; DOI=10.1038/35106579;
MEDLINB=21576510; PubMed=11719806; DOI=10.1038/35106579;
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P.,
Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
Weissenbach J., Vivares C.P.;
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Nature 420:316-320(2002).

EMBL; AL606619; CAE02821.2; -; Ge Gramene; QYXR59; -

GO; GO:0005783; C:endoplasmic ret Interpro; IPR003388; Reticulon.

Pfam; PF02453; Reticulon; 1.

PROSITE; PS50845; RETICULON; 1.

SEQUENCE 199 AA; 22079 MW; BF
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OSUNBA0043A12.26 protein.
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NUCLEOTIDE SEQUENCE:

PubMed=12447439; DOI=10.1038/nature01183;

Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J., Feng Q., Zhang Y., Hao P., Wang S., Fu G., Ying K., Yu S., Tang Y., Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Fan D., Liu Y., Hu T., Li T., Hu H., Guan J., Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D., Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J., Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H., Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y., Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W., Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W., Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gramene;
SEQUENCE
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Sasaki T., Matsumoto T., Katayose Y.,
'Oryza sativa nipponbare(GA3) genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
MCBI_TaxID=39947;
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Submitted (AUG-20
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EMBL; AF538033; AAP31498.1; -; mRNA.

Ensembl; ENSMUSG00000031493; Mus musculus.

RMGI; MGI:2181461; Ggn.

GO; GO:0005737; C:cytoplasm; IDA.

GO; GO:0005730; C:nuclear membrane; IDA.

GO; GO:0005730; C:nucleolus; IDA.

RGO; GO:0005933; F:protein dimerization activity; IDA.

RGO; GO:00046983; F:protein localization; IDA.

RGO; GO:0008104; P:protein localization; IDA.

SEQUENCE 271 AA; 28754 MW; 28A25610172AB42A CRC64;
                                                                                                                                                                                  Complete proteome; Hypothetical protein; Si
SIGNAL 1 24
                                                                                                                                                                                                                                                                 Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatt Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Harrison F.H., Gibson J., Harwood C.S.; "Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris.";
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation updat
Hyporhetical protein precursor.
OrderedLocusNames=RPA1743;
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CGA009 / ATCC BAA-98;
PubMed=14704707; DOI=10.1038/nbt923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
Bradyrhizobiaceae; Rhodop:
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Q6N908;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna
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                                       RPLPPLP 7
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                                                                                 Conservative
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                                                                               Score 41; DB Pred. No. 2.2); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41;
Pred. No.
                                                                                                                                                                   22826BFA24CF75C9
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Mismatches 0;
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role in
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., Tabita E
res J.L., E
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RESULT B
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Q9BEA8; Q9SM04; Q95N10;

28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 48, Last sequence update)

13-SEP-2003 (Rel. 48, Last annotation update)

Tumor necrosis factor ligand superfamily member 6, membrane

[Contains: Tumor necrosis factor ligand superfamily member 6, soluble
       EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
STRAIN=Landrace x Large Yorkshire white; TISSUE=Thymocyte;
STRAINE=21653191; Pubmed=11792426; DOI=10.1010/S0161-5890(01)00098-0;
Motegi-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;
Motegi-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tsuyuki S., Kono M., Bloom E.T.;
"Cloning and potential utility of porcine Fas
in porcine cells protects them from attack by
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21322533; PubMed=11429161; DOI=10.1089/107999001300177493; Muneta Y., Shimoji Y., Inumaru S., Mori Y.; "Molecular cloning, characterization, and expression of porcine Faligand (CD95 ligand) "; Interferon Cytokine Res. 21:305-312(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning and characterization of porcine Fas ligand cDNA."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhu N., Young Y.;
                                                                                                                                               use as
                                                                                                                                                                                                 between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Porcine Fas-ligand gene: with human gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lymphoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=TNFSF6; Synonyms=FASL;
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                              PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                       Immunol. 38:581-586(2002).

PUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3 modulates its effects (By similarity).

SUBUNIT: Homotrimer (Probable).
                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Type II similarity).
                                                                                                                                                                                                                                                                                                           PTM: The soluble
                                                                                                                                                                                                                                                                                                                                         INDUCTION:
                                                                                                                                                                   Swiss-Prot entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
  AB027297; BAB40919.1;
AY033634; AAK56449.1;
AF397407; AAK84408.1;
AB069764; BAB64291.1;
                                                                                                                                             long
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Laurasiatheria; Cetartiodactyla;
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                                                   mRNA.
mRNA.
mRNA.
Genomic_DNA.
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; Suina; Suida
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                                                                                                                                                                                                               collaboration
                                                                                                                                                                                            outstation
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Q9HCNT Q9HCN
ID Q9HCN Q9HCN
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Best Local S
Matches
                             HSSP; Q8NHL6; 1GOX.
Ensembl; ENSG00000088053; Homo s.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 2.
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InterPro; IPR005052; Family.
InterPro; IPR0050536; TNF subf.
PANTHER; PTHR15161; Fag Tigand;
Pfam; PF00229; TNF; 1.
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CARBOHYD
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PRINTS; PRO1234; TNECROSISFCT.
PRINTS; PR01237; TNPC.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
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PROSITE; PS50049; TNF_2; 1.
Apoptosis; Cytokine; Glycop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N7 HUMAN
QƏHCN7 HUMAN PRELIMINARY;
QƏHCN7;
                                                                                                                                                                                                                                     Ezumi Y., Uchiyama T., Takayama H.; Molecular cloning, genomic structu alternative splice forms of the pla glycoprotein VI."; Biochem. Biophys. Res. Commun. 277:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2003 (TrEMBLrel. 24,
Platelet glycoprotein VI-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                        Biochem. Biophys.
EMBL; AB043820; Bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=GPVI
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20483673; PubMed=11027634; DOI=10.1006/bbrc.2000.3624;
                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
     mmunoglobulin domain
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IPR006053;
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llarity 100.0%;
Conservative (
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103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fas_ligand
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the platelet
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N-linked
N-linked
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Signal-anchor for type II membrane
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Extracellular (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor necrosis factor ligand superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poly-Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pro-rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 1;
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> L (in Ref. 4).
-> P (in Ref. 2).
6743DAA1145671FB CRC64;
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                                                                                                                                                                                                             277:27-36(2000) mRNA.
                                                                                                                                                     sapiens
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(GlcNAc...) (Potential)
(GlcNAc...) (Potential)
(GlcNAc...) (Potential)
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                                                                                                                                                                                                                                                                                                                            chromosomal
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                                                                                                                                                                                                                                                                                                 collagen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                               localization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Potential). (Potential).
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RESULT
Q9UIF2
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Best Local S
Matches 7
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01-MAY-2000 (TrEMBLrel. 3), Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Platelet glycoprotein VI precursor (Platelet glycoprotein
Name=gpVI; Synonyms=GPVI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                       P30273:FCERIG; NbExp=1; IntAct=EBI-515278, EBI-515289; P06241:FYN; NbExp=1; IntAct=EBI-515278, EBI-515315; P07948:LYN; NbExp=2; IntAct=EBI-515278, EBI-79452; P07947:YES1, NbExp=1; IntAct=EBI-515278, EBI-515331; EMBL; AB035073; BAA89333.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Platelet
Submitted
                                                                                             CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9UIF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UIF2_HUMAN
                                                                                                                             Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 2.
Immunoglobulin domain;
                                                                                                                                                                                                                                                             PIR; JC7509; JC7509.
                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning, genom alternative splice forms glycoprotein VI.";
                                                                                                                                                                                                                                                                                                                                                                                                             Ezumi Y., Uchiyama T.,
                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
MEDLINE=20483673; PubMed=11027634; DOI=10.1006/bbrc.2000.3624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa;
                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                     HSSP; Q8NHL6;
                                                                                                                                                                                                                                                                                                                                                                Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20483673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
                                                                                                                                                                 InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                                                                                         P; Q8NHL6; IGOX.

ACt, Q9UIF2; -.

GO:0005887; C:integral to plasma membrane;
GO:0005818; F:collagen binding; TAS.
GO:0004888; F:transmembrane receptor activi
GO:0007167; P:enzyme linked receptor protei
                                                                                                                                                                                                                                                                                                                                                 INTERACTION:
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  307
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                                              Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPLPPLP
                     RPLPPLP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycoprotein VI."; (NOV-1999) to the EMBL/GenBank/DDBJ databases
  RPLPPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321
                                                                                              339 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Human)
                                                                                                           21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35158 MW;
                                                                                                                                                                                                                                                                                                                                                                                     genomic structure, cl
forms of the platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euarchontoglires;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                              36923 MW;
                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                               Takayama H.;
                                                                                                                                 Signal
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Pred. No. 2.6
0; Mismatches
                                                ,
,
                                                                                              Potential.
Potential.
4237576E95E030CC
                                                Score 41; DB 2; ...
Pred. No. 2.8e+02;
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93FBF88945958345 CRC64;
                                                                                                                                                                                                                                                                                                                                                              277:27-36 (2000)
                                                                                                                                                                                           receptor activity; TAS. receptor protein signaling pa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339
                                                                                                                                                                                                                                                                                                                                                                                                   chromosomal localization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                      collagen
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                                                                        Length 339;
                                                                                                  CRC64;
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RESULT 11
Q5YME9_NOCFA PRELIMINARY;
ID Q5YME9_NOCFA PRELIMINARY;

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rabey J., Helton E., Jones B.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
RA Garcia R.W., Schmutz J., Wyers R.M.,
RA Garcia R.W., Schmutz J., Wyers R.M.,
RA Garcia R.W., Schmutz J., Wyers R.M.,
RA Ga
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shiba T., Hattori M.;
"The complete genomic sequence of Nocardia farcinica IFM 10152.";
Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
EMBL; AP006619; BAD60642.1; -; Genomic DNA.
GO; GO:0003824; F:catalytic activity; TEA.
GO; GO:0008155; P:metabolism; TEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q5YME9;
25-OCT-2004
25-OCT-2004
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q6PASO XENLA
Q6PASO;
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STRAIN=IFM 10152;
STRAIN=IFM 10152;
PubMed=15466710; DOI=10.1073/pnas.0406410101;
Ishikawa J., Yamashita A., Mikami Y., Hoshino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Corynebacterineae; Nocardiaceae; Nocardia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGC68521 protein.
Name=MGC68521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001354; MR_MLE.
Pfam; PF01188; MR_MLE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nocardia farcinica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=pnf11170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPLPPLP 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPLPPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteome; Hypothetical 378 AA; 39948 MW; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28,
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Last seq
Last ann
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; Plasmid.
251B906460428B4F (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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RESULT
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L. Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K.J., Max., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madna A., Rodrigues S., Sanchez A.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human mid mouse cDNA sequences";

Proc. Matl Acad Sci. II S.A. Gay L.E., 16003 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
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Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Xenopus laevis (Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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25-OCT-2004 (TrembLrel.
25-OCT-2004 (TrembLrel.
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"Genetic and initiative."
                                                           Richardson P.;
                                                                                        Klein S.L.,
                                                                                                                 MEDLINE=22341132;
                                                                                                                                                    TISSUE=Oocytes
                                                                                                                                                                                NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Kidney;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Richardson P.;
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                                                                                  Strausberg
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                                                                                  PubMed=12454917;
sberg R.L., Wagne;
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Last sequence update)
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Pred. No. 3.3
0; Mismatches
                                                                                                                                                                                                                                      99:16899-16903 (2002)
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                            Xenopus
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                                                                                  DOI=10.1002/dvdy.10174;
r L., Pontius J., Clifton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404
                            research:
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RESULTT Q872X22 ID 72X2 Q8 AC Q8 DT 011 DT 0
      RESULT 15
QBIRH4 DROME
ID QBIRH4;
DT 01-MAR-2
DT 01-MAR-2
DT 01-MAR-2
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DT CG9181-B
GN Name-Dtp
GN Name-Dtp
OS Drosophi
OC Eukaryot
OC Neoptera
OC Ephydroi
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RP NUCLEOTI
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RA Adams M.
RA Amanatid
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Best Local :
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Best Local
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QBIRH4;
QBIRH4;
QBIRH4;
QBIRH4;
QBIRH4;
QBIRH4;
QBIRH2003 (TIEMBLIE1. 23, Las
Q1-MAR-2003 (TIEMBLIE1. 26, Las
Q1-MAR-2004 (TIEMBLIE1. 26, Las
CG9181-PD, 180-form D.
Name=Ptp61F; ORFNames=CG9181;
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X2 NEUCR
Q872X2 NEUCR I
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Klein S. Strausberg R.;
Submitted (JUL-2004) to the
EMBL; BC076858; AAH76858.1;
SROHENCE 404 AA; 44557 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
Hypothetical protein B23B10)
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Klein S., Strau
NUCLEOTIDE SEQUENCE:
NUCLEOTID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                German Neurospora genome project;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ
EMBL; BX284752; CAD70439.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 423 AA; 48356 MW; BAEB36BEA38D1CE
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Schulte U., Aign V.,
Nyakatura G., Mewes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetidae; Sordariales; Sordariaceae;
NCBI_TaxID=5141;
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                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
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RA Brandon R.C., Mortman J.K., Fanderi R.D., Linany W., Chen, RA Wan K.H., Doyle C. Baxter E.G., Halt G., Champe M., Pfeliffer B.D., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Balew R.M., Basu A., Baxendale J., Bayraktaroglu L., Belshakov S., RA Balew R.M., Basu A., Baxendale J., Bayraktaroglu L., Belshakov S., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houtek J., RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kull Doywam C., RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kull D., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Messen D.L., Masken P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., RA Mentert K., Ranington K., Saunders R.D.C., Scheeler F., Shen H., RA Spier E., Spradling A.C., Stapleton M., Strong R., Boyler E., Spradling A.C., Stapleton M., Strong R., Bung A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weinsenbach J., Ra Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weinsenbach J., Wang X., Yeb R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Pile genome sequence of Drosophila melanogaster.";

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Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B
Bettencourt B.R., Celniker S.E., de Gr.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Kaminker J.S., Bergman
Patel S., Frise E., Who
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NUCLEOTIDE SEQUENCE.
Berkeley Drosophila Genome Projecelniker S., Carlson J., Wan K.,
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Genome Biol.
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RA HOSKINS R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E., RA YU C., Rubin G.; Rubin G.; Purosophila melanogaster release 4 sequence."; RI Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. RN [6]

RN HUCLEOTIDE SEQUENCE.

RR HUCLEOTIDE SEQUENCE.

RR HUSEN ENDO1471; AANI1476.1; -; Genomic_DNA.

RR HUSE, PED011; DOWSOPHILA melanogaster.

DR HUSE, PED011; DOWSOPHILA melanogaster.

DR HUSE, PED0100313B; CG9181.

DR F1yBase; FE90000313B; CG9181.

DR F1yBase; FE90000313B; CG9181.

DR F1yBase; FE90000313B; CG9181.

DR F1yBase; FE90000313B; CC9VCoplasm; IDA.

DR F1yBase; FE90000313B; PED61E.

DR F1yBase; FE9000031B; PED61E.

DR F1yBase; FE900031B; PED61E.

DR G0; G0:000647D; P: protein amino acid dephosphorylation; IDA.

DR G0; G0:000647D; P: protein amino acid dephosphorylation; IDA.

DR G0; G0:000647D; P: protein amino acid dephosphorylation; IDA.

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ABG67199	AAU04058	AAB85268	ABB11582	AAW79159	ADU83369	ADG32003	AAE39509	AAE23218	AAU77542	AAO09572	ABP70948	ADH22377	ADK98541	AAW17009	AAW25378	AAW05068	AAR93467	AAR93547	AAR93548	ABM87190
Abg67199	Aau04058	Aab85268	Abb11582	Aaw79159	Adu83369	Adg32003	Aae39509	Aae23218	Aau77542	Aao09572	Abp70948	Adh22377	Adk98541	Aaw17009	Aaw25378	Aaw05068	Aar93467	Aar93547	Aar93548	Abm87190
Human	Human int	Human IL-	Human cla	Zcytor7 c	Human rec	Cow lung-	Bovine RA	Cow recep	Bovine re	Human pol	Interleuk	Human rec	Human imm	SH3			GST-SRC p	Random 10	Random 10	Rice abio

ALIGNMENTS

RESULT 1 AAB17230

AAB17230;

AAB17230 standard; peptide; 7 AA.

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Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; II-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                           23-OCT-1998;
22-OCT-1999;
                                                                                                                                                   Feige U,
                                                                                                                                                                        (AMGE-) AMGEN INC.
                                                                                                                                                                                                                         25-OCT-1999;
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                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                           thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                           SH3 antagonist peptide sequence SEQ ID NO:286.
                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-2000
                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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99US-00428082
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                                                                                                                                                    Cheetham
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                                                                                                                                                    Boone
                                                                                                                                                   TC;
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The present invention describes composition of matter (I) comprising a Fc domain, pharmacologically active peptides, and linkers. Where (I) i (XI)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L3)e-P3, or -(L1)c-P1-(L3)e-P3-(L3)e-P3, or -(L1)c-P1-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P1-(L3)e-P3-(L3)e-P3-(L3)e-P1-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P1-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P1-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P1-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P1-(L3)e-P3-(

Ly active

is:

Claim 39; Page 297; 608pp; English.

active

composition of matter comprising an Fc peptides, useful for treating cancer a

domain and pharmacologically and autoimmune diseases.

WPI; 2000-350702/30.

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The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-[1-(X2)b, where: F1 = an Fc domain; X1 and X2 = act) independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppressive; SPÖ; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; Minibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17231 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified peptide; therapeutic agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SH3 antagonist peptide sequence SEQ
                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                               WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                          23-OCT-1998;
22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombosis;
                                                                                                                                                                                                                                                                                                                            (AMGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease; cytostatic; antiasthmatic
immunosuppressive; EPO; TPO; CTLA4; mimetic;
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                                                                                                                                                                                                               composition of matter comprising an Fc domain and pharmacologically e peptides, useful for treating cancer and autoimmune diseases.
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                                                                                                                                                                                                                                                                                             Liu
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiasthmatic;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; erythropoletin; TPO; tumour necrosis factor alpha inhibitor; TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7
                                                                                                                                             Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
                                                                                                                                                                                                              Feige
                                                                                                                                                                                                                                                                                             02-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                               neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; anaemia; thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmologiantianaemic; anorectic; antiinfertility; haemostatic; dermatological;
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                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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                                                                                                                                retinopathy,
                                                                                                                                                                                                               Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                 syndrome.
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                                                                                                                                   infertility.
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The present invention describes a vehicle-peptide molecule (I) or its multimers. (I) can have antiinflammatory, antitumour, immunosuppressive, cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological, antianaemic, anorectic, antiinfertility, haemostatic, dermatological and

Claim

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Page

55; 176pp;

English.

neuroprotective activities. (I) caprophylactic agent as well as for diagnosing diseases characterised

characterised by

can be used as a therapeutic for screening purposes. (I) is sed by dysfunction of their ass

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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interest, as a part of diagnostic kit to detect the presence of their proteins of interest in a biological sample. Additionally, (I) is useful for treating inflammatory and autoimmune diseases, tumour growth, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders, infertility, and neurological degenerative diseases. (I), comprising EPO-mimetic compounds are useful for treating disorders characterised by low red blood cell levels such as anaemia. The TPO-mimetic comprising compounds are useful for treating conditions that involve an existing megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic tumour which result in thrombocytopaenia, aystemic lupus erythematosus, and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777 represent amino acid and nucleic acid sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                    erythropoletin; TPO; tumour necrosis factor alpha inhibitor; TMP; TNF-alpha inhibitor; interleukin 1 antagonist; TL-1 antagonist; TMP; TPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; antianemic; anorectic; antiinferrility; haemostatic; dermatological; neuroprotective; inflammatory dieease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; anaemia;
                                         Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
                                                                                                                                                  Feige U,
                                                                                                                                                                                                                  03-MAY-2000; 2000US-00563286
                                                                                                                                                                                                                                                    02-MAY-2001; 2001WO-US014310
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                                                                                                                                                                                                                                                                                                                        WO200183525-A2
                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                              Fanconi's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified peptide; mimetic; Fc domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Src homology3 (SH3) antagonist peptide SEQ ID NO:287.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB73224 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           chrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein of interest,
                                                                                                                2002-130313/17.
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                                                                                                                                                                                    AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 7; Conserv
                                                                                                                                               Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                            syndrome.
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                                                                                                                                                                                    INC.
                                                                                                                                                  Cheetham JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41;
Pred. No.
                                                                                                                                                  Boone TC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fusion;
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                                                                                                                                                  Gudas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoglobulin G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IgG;
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Claim 39;

Page 55;

176pp; English

This invention relates to novel mammalian CDR mimetibodies, specific

831; 97pp; English

Disclosure; SEQ ID NO

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RESULT 5
ADJ73377
888888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC neuroprotective activities. (I) can be used as a therapeutic or CC prophylactic agent as well as for screening purposes. (I) is useful for CC diagnosing diseases characterised by dysfunction of their associated CC protein of interest, for identifying normal or abnormal proteins of CC interest, as a part of diagnostic kit to detect the presence of their CC proteins of interest in a biological sample. Additionally, (I) is useful CC for treating inflammatory and autoimmune diseases, tumour growth, cancer, CC infertility, and neurological degenerative diseases. (I) comprising EPO-CC mimetic compounds are useful for treating disorders characterised by low cred blood cell levels such as anaemia. The TPO-mimetic compounds are useful for treating conditions that involve an existing CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic tumour which result in thrombocytopaenia, systemic lupus erythematosus, and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777 crepresent amino acid and nucleic acid sequences used in the
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Best Local S
Matches 7
                                                                                    New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding regiuseful for preparing a composition for treating e.g., immune,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mimetic; CDR mimetibody; gene therapy; transgenic; immune;
cardiovascular; infectious; malignant; neurologic disease; anaemia;
immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a vehicle-peptide molecule (I) or its multimers. (I) can have antiinflammatory, antidumour, immunosuppressive, cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological antianaemic, anorectic, antiinfertility, haemostatic, dermatological and neuroprotective activities. (I) can be used as a therapeutic or prophylactic agent as well as for screening purposes. (I) is useful for
                                                                        cardiovascular
                                                                                                                                                                                                     Heavner GA,
                                                                                                                                                                                                                                                                             29-MAR-2002; 2002US-0368791P
                                                                                                                                                                                                                                                                                                                  24-MAR-2003; 2003WO-US009139
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SH3 antagonist
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ73377;
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                                                                                                                                                                                                                                          (CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                             WO2003084477-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ73377 standard; peptide; 7
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                                                                                                                                                                2003-804237/75.
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7; Conserv
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                                                                                                                                                                                                   Knight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide sequence SeqID 831.
                                                                      or neurologic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the present invention
                                                                                                                                                                                                     DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 41; DB 5; 100.0%; Pred. No. 2e+06;
                                                                                                                                                                                                     Scallon BJ,
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                                                                                                         region,
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RESULT 6
ADJ73378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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cardiovascular; infectious; malignant; neurologic disease; anaemia;
immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
This invention relates to novel mammalian CDR mimetibodies, specific portions or variants thereof. Specifically, it refers to an antibody fragment where a protein has been inserted into, or replaces a portion of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which theelf comprises at least one human framework region and at least one ligand binding region (LBR). The present invention describes human mimetibodies, including modified immunoglobulins and cleavage products
                                                                                                                                                                                                                                                                                                                                                  New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region, useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
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                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 832; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2003-804237/75.
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    832.
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RESULT 7
ADJ53012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        char can be useful in gene therapy and the generation of transgenic plants and animals. Furthermore, the CDR mimetibody is useful for preparing compositions for modulating, treating or reducing the symptoms of immune, cardiovascular, infectious, malignant and/ or neurologic diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, cardiant, antimicrobial, cytostatic and neuroprotective activities. This peptide sequence is an SH3 antagonist peptide sequence used to make a mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypotensive; neuroprotective; nootropic; antibacterial; virucide; fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hypertension; heart failure; neurodegenerative; multiple sclerosis; dementia; Albeimer's disease; anaemia;
which encode them), compositions, methods and uses. The invention may be useful for the development of compounds with an immunosuppressive, cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, antibacterial, virucide or fungicide activity. In addition, the disclose sequences may prove useful for gene therapy. The CH1-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell, tissue, organ or animal, specifically for modulating, treating, alleviating, preventing the incidence or reducing the symptoms of an immune, cardiovascular (for example arrhythmia, hypertension or heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7
                                                                                                                                                                                                                                                                                                         WPI;
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                                                                                                                                                                                                                                     New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, or neurodegenerative disease or disorder, anemia, cancer, or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUN-2002; 2002US-0392431P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancerous condition; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CH1 deleted mimetibody-related peptide SeqID832.
                                                                                                                                                                                      Claim 3;
                                                                                                                                                                                                                       diseases.
                                                                                                                                                                                                                                                                                                                                          Kutoloski
                                                                                                                                                                                                                                                                                                                                                           Heavner
                                                                                                                                                                                                                                                                                                                                                                                          (CENZ )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                         invention relates to CH1 deleted mimetibodies (and the DNA sequences 
h encode them), compositions, methods and uses. The invention may be
                                                                                                                                                                                                                                                                                                          2004-082870/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RPLPIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 7; Conserve
                                                                                                                                                                                                                                                                                                                                                         GA,
                                                                                                                                                                                                                                                                                                                                                                                            CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPLPIPP 7
                                                                                                                                                                                    SEQ ID NO 832; 129pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
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                                                                                                                                                                                                                                                                                                                                                         Knight
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2003WO-US020347.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fungal infection.
                                                                                                                                                                                                                                                                                                                                                           DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                           Ghrayeb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ⋛
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                                                                                                                                                                                                                                                                                                                                                           Scallon BJ,
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Best Local S
Matches 7
                     This invention relates to CH1 deleted mimetibodies (and the DNA sequences which encode them), compositions, methods and uses. The invention may be useful for the development of compounds with an immunosuppressive, cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, antibacterial, virucide or fungicide activity. In addition, the disclosed sequences may prove useful for gene therapy. The CH1-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell, tissue, organ or animal, specifically for modulating, treating, tissue, organ or animal, specifically for modulating, treating, alleviating, preventing the incidence or reducing the symptoms of an immune, cardiovascular (for example arrhythmia, hypertension or heart failure), or neurodegenerative (for example multiple sclerosis, dementia or Alzheimer's disease) diseases or disorders, anaemia, cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                failure), or neurodegenerative (LVL CONTERED AND ADDRESS) or Alzhaimer's disease) diseases or disorders, anaemia, cancerous or Alzhaimer's diseases (for example bacterial, viral or conditions, or infectious diseases (for example bacterial, viral or fungal infection). The present sequence is that of a peptide which may fungal infection). The present sequence is that of a peptide which may read during the creation of a mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New CH1-deleted mimetibody polypeptides and nucleic acids, useful modulating, treating, alleviating, preventing an immune, cardiovas or neurodegenerative disease or disorder, anemia, cancer, or infec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multiple sclerosis; dementia; Alzheimer's disease; cancerous condition; infectious disease; bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant; hypotensive; neuroprotective; nootropic; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   greeses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heavner GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004002417-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ53011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2004-082870/08
                                                                                                                                                                                                                                                                                                                                                                                                                        3; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                  831; 129pp;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorder; cardiovascular di
failure; neurodegenerative;
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2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anemia, cancer, or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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infectious

diseases

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antiinflammatory, neurole respiratory-Gen activity

This invention relates to CH1 deleted mimetibodies (and the DNA sequences which encode them), compositions, methods and uses. The invention may be useful for the development of compounds with an osteopathic, cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen, gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic, immunomodulator, antiallergic, muscular-Gen, cytostatic,

Gen, gymaecological-Gen, hepatotropic, antiallergic, muscular-Gen, cytostatic neuroleptic, ophthalmological, nephro

cytostatic,

nephrotropic

Claim 15;

SEQ ID NO 832; 123pp; English.

nutritional disorders.

neurologic

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWF; cytokine; bone disorder; joint disorder; cardiovascular disorder; dental disorder; oral disorder; dermatological disorder; ear disorder; nose disorder; troat disorder; endocrine disorder; metabolic disorder; gastrointestinal disorder; gynaecological disorder; hepatic disorder; obstetric disorder; haematologic disorder; munnological disorder; allergic disorder; infectious disorder; musculoskeletal disorder; oncological disorder; neurological disorder; pediatric disorder; psychiatric disorder; ophthalmologic disorder; pediatric disorder; psychiatric disorder;
                                                                                                                                                  New CH1 deleted mimetibody polypeptide and nucleic acid, useful diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic
                                                                                                                                                                                                                                                                                             28-JUN-2002; 2002US-0392431P
19-SEP-2002; 2002US-0412144P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; gynaecological-Gen; hepatotropic; haemostatic; immunomodulator; antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fungal infection). The present sequence is that of a peptide which may be used during the creation of a mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                   30-JUN-2003; 2003WO-US020495
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                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ophthalmological; nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CH1 deleted mimetibody; osteopathic; cardiovascular-Gen;
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                                                                                                                                                                                                                                                                   (CENZ ) CENTOCOR INC.
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7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; peptide;
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ADJS17 20
ADJS1 ADJS1 XX
AC ADJS1 XX
DT 06-MJ
XX CH1 c
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XX
VINF;
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KW ONCOl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; gynaecological-Gen; hepatotropic; haemostatic; immunomodulator; antiallergic; muscular-Gen; cytostatic; antiallammatory; neuroleptic; ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor; TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder; dental disorder; oral disorder; dermatological disorder; ear disorder; nose disorder; throat disorder; endocrine disorder; metabolic disorder; gastrointestinal disorder; gynaecological disorder; hepatic disorder; obstetric disorder; haematologic disorder; immunological disorder; allergic disorder; neurological disorder; nutritional disorder; ophthalmologic disorder; pediatric disorder; psychiatric disorder; pulmonary disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ51972 standard; peptide; 7
                                                                                      New CH1 deleted mimetibody polypeptide and nucleic acid, useful for diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic and
                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUN-2002;
19-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CH1 deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004002424-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CH1 deleted mimetibody; osteopathic; cardiovascular-Gen;
                                                                nutritional disorders.
                                                                                                                                                                                                                      WPI; 2004-082872/08.
                                                                                                                                                                                                                                                                                Kutoloski KA;
                                                                                                                                                                                                                                                                                                                Heavner GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2003; 2003WO-US020495
                                                                                                                                                                                                                                                                                                                                                                          (CENZ )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۳
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                                                                                                                                                                                                                                                                                                                                                                             CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPLPIPP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mimetibody-related peptide SeqID831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                          Knight DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                    2002US-0392431P.
2002US-0412144P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                Ghrayeb J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 8;
Pred. No. 2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
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                                                                                                                                                                                                                                                                                                             Scallon
                                                                                                infectious, neurologic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                             Nesspor TC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>0</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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Claim 15; SEQ ID NO 831; 123pp; English

Identifying polypeptide(s) having specific functional domain (esp.

SH3

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RESULT 11
AAW05415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modulator or cytokine-agonist. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of the CHI deleted minetibody, such as a bone or joint, cardiovascular, dental or oral, dermatological, ear, nose or throat, endocrine, metabolic, gastrointestinal, gynaecological, hepatic, obstetric, haematologic, immunological, allergic, infectious, pediatric, psychiatric, renal or pulmonary disorders. The present sequence is that of a peptide which may be used during the creation of a
                                                                                                                                                                                                                                                                                                        cellular signalling element; cellular structural element; mal protein identification; functional domain; protein screening; cellular signal transduction process; binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW05415 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mimetibody of the invention.
                    WPI; 1996-465045/46
                                          Sparks AB,
                                                                                                 07-APR-1995;
03-APR-1996;
                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                          Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;
                                                                                                                                                                                                                                                                                                                                                                  Src SH3 domain-binding peptide, T12SRC.4.
                                                                                                                                                                                                                                                                                                                                                                                          24-FEB-1998
                                                                                                                                    04-APR-1996;
                                                                                                                                                          10-OCT-1996.
                                                                                                                                                                                 WO9631625-A1
                                                                                                                                                                                                                                         Modified-site
                                                                 (CYTO-) CYTOGEN CORP. (UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to CH1 deleted mimetibodies (and the DNA sequences
h encode them), compositions, methods and uses. The invention may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RPLPIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPLPIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,
                                            Hoffman N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                  95US-00417872
96US-00630915
                                                                                                                                    96WO-US004454
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                      /note= "C-terminal amide"
                                                                                                                                                                                                                              'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                              "Biotin labelled"
                                          кау вк,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 8;
Pred. No. 2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                             Fowlkes DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 8;
                                            Mcconnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                              S
                                                                                                                                                                                                                                                                                                                                   malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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regardless of sequence homology

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RESULT 12
AAW05482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                  Src-homology region 3 domain; human; mouse; SH3 domain; cell growth; cellular signalling element; cellular structural element; malignancy; protein identification; functional domain; protein screening;
WPI; 1996-465045/46
                                                                                                                                                07-APR-1995;
03-APR-1996;
                                                                                                                                                                                                              04-APR-1996;
                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SH3-binding peptide T12SRC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW05482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW05482 standard; peptide; 13
                                                                               (CYTO-)
                                                                                                                                                                                                                                                        10-OCT-1996
                                                                                                                                                                                                                                                                                                  W09631625-A1
                                                                                                                                                                                                                                                                                                                                                                                  cellular signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regardless
                                          AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RPLPIPP 7
                                                                                  CYTOGEN CORP.
UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - comprises detecting selective binding to recognition unit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPLPIPP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of sequence homology.
                                       Hoffman N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                              95US-00417872
96US-00630915
                                                                                                                                                                                                              96WO-US004454
                                                                                                                                                                                                                                                                                                                                                                                transduction process; binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 41; Di
100.0%; Pred. No. 19;
tive 0; Mismatches
                                          Kay BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English
                                          Fowlkes DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DВ
19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ب</u>
                                          Mcconnel1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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밁 S

Identifying polypeptide(s) having specific functional domain (esp. SH3 domain) - comprises detecting selective binding to recognition unit,

AAW16949-W16950 are peptides that bind

to the Src SH3 domain.

The

SH3

Disclosure; Page 24;

116pp;

English.

Peptide with binding affinity for Src homology region 3 (SH3) domains proteins - useful for e.g. modulating signal transduction pathways at cellular level, esp. protein tyrosine kinase-mediated.

the

WPI; 1996-117151/12.

Sparks

кау вк,

Thorn JM,

Quilliam

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(UYNC-) UNIV NORTH CAROLINA.

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RESULT 13
AAW16949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC AAW05445-W05492 represent Src-homology region 3 (SH2) domain binding CC peptides. These sequences were used as parts of multivalent recognition CC unit complexes used in the method of the invention. The method of the CC invention is for identifying polypeptides containing functional domains of interest (especially SH3 domains). It comprises contacting a CC multivalent recognition unit (RU) complex with a number of peptides and CC identifying polypeptides having a selective binding affinity for the RU complex. The method is based on functional similarities and does not rely CC complex. The method is based on functional similarities and does not rely CC enteritying proteins containing an SH3 domain due to the minimal sequence identifying proteins containing an SH3 domain due to the minimal sequence CC homology among known SH3 proteins. Multivalent RU complexes are CC particularly suited to screening for polypeptides containing functional CC domains that are similar to, but not identical in sequence to, the CC original target functional domain. The new method enables proteins having CC a common function to be identified. Identification of novel SH3 proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                          22-JUL-1994;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                         Src; SH3; Src homology region 3; binding affinity; oncogenic protein; protein tyrosine kinase; signal transduction; RNA processing; translation.
                                                                                                                                                                                                                                                                                                             08-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Src SH3 domain-binding peptide used in signal transduction modulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        will be useful for a better understanding of cell growth, malignancy, signal transduction processes, etc. New candidate drugs can be identified, and their specificities (e.g. pharmacological activities) be assessed using the method of the invention
                                                                                                                                                                                                                                                                            24-JUL-1995;
                                                                                                                                                                                                                                                                                                                                           WO9603649-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW16949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW16949 standard; peptide; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Fig 13; 174pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RPLPIPP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPLPIPP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ĀΑ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                          94US-00278865
95US-00483555
                                                                                                                                                                                                                                                                            95WO-US009382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>,,</u>
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RESULT 14
AAW11101
ID AAW11
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Best Local S
Matches 7
Query Match
Best Local Similarity
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                                                                                                                                       for regulating the processing, trafficking or translation of RNA. Conjugates of the peptides with detectable labels or imaging agen useful for imaging cells, tissues and organs in which Src or Src-
                                                                                                                                                                                                      AAW11098-W11124 are peptides that bind to the Src SH3 domain. The SH3 binding peptides are useful in modulating signal transduction pathways at the cellular level (especially protein tryosine kinase-mediated), modulating oncogenic protein activity, or providing compounds for the development of drugs with the ability to modulate broad classes, as well as specific classes, of proteins involved in signal transduction and also as specific classes, of proteins involved in signal transduction and also
                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide with binding affinity for Src homology region 3 (SH3) domains proteins - useful for e.g. modulating signal transduction pathways at cellular level, esp. protein tyrosine kinase-mediated.
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07-JUN-1995;
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                                                                   Sequence
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RPLPIPP

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RESULT 15
AAW25514
ID AAW25
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                                                                                                                The present sequence represents a Src SH3 synthetic binding peptide. SH3 CC (Src homology region 3) binding peptides are selected from: (a) peptides CC which bind the SH3 domain of Cortactin; (b) peptides which bind the CC middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; CC (d) peptides which bind the SH3 domain of Abl; CC (d) peptides which bind the SH3 domain of Abl; CC (d) peptides which bind the SH3 domain of ELC gamma; (f) peptides which bind the SH3 domain of CK; (e) peptides which bind the SH3 domain of CK; (h) peptides which bind the SH3 domain of CTs; (e) peptides which bind CC peptides which bind the SH3 domain of CTs; (e) peptides which bind CC the amino-terminal SH3 domain of CTs; (h) peptides which bind CC the amino-terminal SH3 domain of GTs2. The purified binding peptides can CC be used in the method to identify inhibitors of their binding to their CT respective SH3 domains, which could be used to modulate the SH3 CC domain. The peptides can also be used to modulate the SH3 CC domain. The peptides can also be used to activate STC or STC-related CT protein tyrosine kinases, to stimulate the immune response by increasing the production of certain lymphokines, e.g. tumour necrosis factor-alpha CC and interleukin-1, or to deliver a conjugated molecule to certain CC cellular compartments containing STC or STC related proteins
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Rider JE;
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negative regulator	kinase-binding pro	probable carotenoi	spliling factor SR	Fas ligand - mouse	_	hypothetical prote	proline-rich prote	hypothetical prote	probable two-compo	hypothetical prote	hypothetical prote	ERG-associated pro	hypothetical prote	double-stranded RN	hypothetical prote

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hypothetical prote probable exported conserved hypothet bilirubin oxidase hypothetical prote hnf-3/forkhead tra
                                                                        C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 31-Dec-2004
C;Accession: B41224
C;Accession: B41224
R;Kennedy, M.A.; Gonzalez-Sarmiento, R.; Kees, U.R.; Lampert, F.; Dear, N.; Boehm, Proc. Natl. Acad. Sci. U.S.A. 88, 8900-8904, 1991
A;Title: HOX11, a homeobox-containing T-cell oncogene on human chromosome 10q24.
A;Reference number: A41224; MUID:92020958; PMID:1681546
A;Accession: B41224
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-284 <KEN>
A;Cross-references: UNIPROT:Q61663; UNIPARC:UPI00002338B; GB:M75953; NID:g193843; C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;158-214/Domain: homeobox homology <HOX>
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A;Cross-references: GDB:370911
C;Superfamily: fos transforming protein; fos/jun DNA-binding domain homology C;Keywords: DNA binding; transcription regulation
F;122-162/Domain: fos/jun DNA-binding domain homology <FJD>
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A;Molecule type: mRNA
A;Residues: 1-222 <HA3>
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hypothetical protein 1 - Xanthomonas sp. transposon Tn5053 (fragment)
c;Species: Kanthomonas sp.
c;Species: Kanthomonas sp.
c;Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 11-Jan-2000
c;Accession: S32799
c;Accession: S32799
R;Kholoddi, G.Y.; Yurieva, O.V.; Lomovskaya, O.L.; Gorlenko, Z.M.; Mindlin, S.Z.; Nikifc
J. Mol. Biol. 230, 1103-1107, 1993
A;Title: Tn5033, a mercury resistance transposon with integron's ends.
A;Reference number: S32795; MUID: 33253772; PMID: 8387603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q28173; UNIDARC:UDI00001330EE; GB:M91212; NID:g163650; PIDN: A;Experimental source: lung
A;Note: sequence extracted from NCBI backbone (NCBIP:109436)
A;Note: sequence extracted from NCBI backbone (NCBIP:109436)
A;Note: parts of this sequence, including the amino end of the mature protein, were dete
R;Schmidt, A.M.; Vianna, M.; Gerlach, M.; Brett, J.; Ryan, J.; Kao, J.; Esposito, C.; He
J. Biol. Chem. 267, 14987-14997, 1992
A;Title: Isolation and characterization of two binding proteins for advanced glycosylati
A;Reference number: A42878; MUID:92340546; PMID:1321822
A;Reference number: A42878; MUID:92340546; PMID:1321822
A;Residues: 23-24,'X',26-37,'X',39-49,'XX',52-54 <8CH>
A;Cross-references: UNIPARC:UDI00000876EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  advanced glycosylation end-products receptor precursor - bovine
NyAlternate names: advanced glycosylation end product-binding protein, 35K;
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Mar-1993 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004
C;Accession: A42879; A42878; S27949
C;Accession: A42879; A42878; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Ell:
J. Biol. Chem. 267, 14998-15004, 1992
A;Title: Cloning and expression of a cell surface receptor for advanced glycosylone and expression of a cell surface receptor Advanced glycosylone and expression of a cell surface receptor for Advanced glycosylone and expression of a cell surface receptor for Advanced glycosylone and expression of a cell surface receptor for Advanced glycosylone and expression of a cell surface receptor for Advanced glycosylone and expression and expression of a cell surface receptor for Advanced glycosylone and expression and expression and expression and expression and expression and expression of a cell surface receptor for advanced glycosylone and expression and expression and expression and expression of a cell surface receptor for advanced glycosylone and expression 
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    맑
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A;Description: neuronal receptor for amphoterin, a DNA-binding protein involved in neur C;Superfamily: advanced glycosylation end products receptor; immunoglobulin homology C;Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein F;1-22/Domain: signal sequence #status predicted <SIG>F;23-416/Product: advanced glycosylation end-products receptor RAGE #status predicted <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S32799
                                                                                                                                                                                                                                                                                                                              C;Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glyco cellular function, thus contributing to tissue lesions in diabetes.
C;Comment: This receptor appears also to mediate the effects of amyloid beta peptide on
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                                                                                                                                                                                                                                                   C; Function:
                                                                                                                                                                                                                                                                                           ates in the neurotoxic pathway that produces dementia in Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: endothelial cells
A; Note: sequence extracted from NCBI backbone (NCBIP:109434)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-416 < NEE>
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Pred. No.
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F;31-100/Domain: immunoglobulin homology <IM1>
F;136-209/Domain: immunoglobulin homology <IM2>
F;262-313/Domain: immunoglobulin homology <IM3>
F;262-313/Domain: immunoglobulin homology <IM3>
F;355-372/Domain: immunoglobulin homology <IM3>
F;355-372/Domain: intracellular #status predicted <TMM>
F;373-416/Domain: intracellular #status predicted <INT>
F;373-416/Domain: intracellular #status predicted <INT>
F;375,80/Binding site: carbohydrate (Asn) (covalent) #status
F;38-98,143-207,269-311/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transforming protein (cbl) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 17-Mar-1999
A; Molecule cypu. A; Residues: 1-1267 < WI2>
A; Cross-references: UNIPARC: UPI0000083350;
A; Cross-references: Clone F45H11
                                                                                                                                                                                                                                      A;Residues: 1-1267 <WIL>
A;Cross-references: UNIPROT:Q93564; UNIPARC:UPI0000083350; EMBL:Z78418; PIDN:CAB01699.1
A;Experimental source: clone F25D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F45H11.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: I5-Oct-1999 #sequence revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oncogene 6, 653-657, 1991
A;Title: The sequences of the human and mouse c-cbl proto-oncogenes show v-cbl was A;Reference number: A43817; MUID:91232862; PMID:2030914
A;Accession: B43817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: B43817
R;Blake, T.J.; Shapiro, M.; Morse III, H.C.; Langdon,
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                                                                                                                                            A; Reference number:
A; Accession: T22252
                                                                                                                                                                  submitted to the EMBL Data A; Reference number: Z19537
                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data A; Reference number: Z19409 A; Accession: T21340
                                                                                                                                                                                                                                                                                                                                                                                                                                     R; McMurray, A.
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A; Residues: 1-896 < BLA>
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                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
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85.7%;
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85.7%;
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    Mismatches

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Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 2;
Pred. No. 1.6e+02
                                                                                                                                                                                         August
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                               EMBL: Z78420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W.Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                  PIDN: CAB01711.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                  GSPDB: GN00019
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90/2;

149/3; 207/1; 356/2; 413/2;

458/2; 520/3; Length 1267;

691/3;

777/2; 796/2;

92.7%;

Score

38;

DB Ν --

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F;108-131/Domain: transmembrane #e
F;140-158/Jomain: transmembrane #e
F;212-234/Domain: transmembrane #e
F;212-234/Domain: transmembrane #e
F;328-350/Domain: transmembrane #e
F;468-466/Jomain: transmembrane #e
F;469-50/Domain: transmembrane #e
F;577-596/Jomain: transmembrane #e
F;659-67/Jomain: transmembrane #e
F;659-67/Domain: transmembrane #e
F;617-834/Domain: transmembrane #e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;1169-1188/Domain: transmembrane #status predicted <TR23>
F;1197-1215/Domain: transmembrane #status predicted <TR23>
F;1291-1310/Domain: transmembrane #status predicted <TR24>
F;1377-1402/Domain: transmembrane #status predicted <TR24>
F;99,102,274,470,813,1157,1269,1485,1703,1713,1745,1760,1848/Binding site: carbohydrate
F;99,102,274,470,813,1157,1269,1485,1703,1713,1745,1760,1848/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted carbohydrate (Ser) (covalent) (by cAMP-dependent kinase)
                                                 E4 protein - human papillomavirus type 51
c;Species: human papillomavirus type 51
A;Note: host Homo sapiens (man)
c;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
c;Accession: C40415
R;Lungu, O.; Crum, C.P.; Silverstein, S.J.
J. virol. 65, 4216-4225, 1991
A;Title: Biologic properties and nucleotide sequence analysis of human papi:
A;Reference number: A40415, MUID:91303675; PMID:1649326
A;Accession: C40415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;11057-1084/Domain: transmembrane #status predicted <TR18>
F;1135-1153/Domain: transmembrane #status predicted <TR19>
F;1169-1188/Domain: transmembrane #status predicted <TR20>
F;1197-1215/Domain: transmembrane #status predicted <TR21>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Grabner, M.; Friedrich, K.; Knaus, H.G.; Striessnig, J.; Scheffauer, Proc. Natl. Acad. Sci. U.S.A. 88, 727-731, 1991
A;Title: Calcium channels from Cyprinus carpio skeletal muscle. A;Reference number: A37860; MUID:91126068; PMID:1846962
A;Accession: A37860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Cyprinus carpio (common carp)
C;Date: 31-May-1991 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: A37860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-1852 < GRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
A37860
                          A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   calcium channel
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                               1832 RPIPVPP 1838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RPLPIPP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPLPIPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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71.4%;
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| <TR08>
| <TR09>
| <TR11>
| <TR12>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                   human papillomavirus
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T16001
                                                                                                                                                A; Map position:
                                                                                                                                                                          A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Chissoe,
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Best Local
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hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G86197
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonsv
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, (C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-383 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, September 1995 A;Description: The sequence of C. elegans cosmid F A;Reference number: Z18444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F09E5.12 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep_1999 #sequence_revision 20-Sep_1999 #text_change 09-Jul-2004 C;Accession: T16001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P26548; UNIPARC:UPI0000138387; GB:M62877 C;Superfamily: papillomavirus E4 protein C;Keywords: early protein
                                                                                                                                                                                                         A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q19261; UNIPARC:UPI00000826A8; EMBL:U37429; NID:g1019949;
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-312 <C
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es 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 RPIPLPP 30
  Similarity
5; Conserv
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RPIPLPP 261
       Conservative
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                                                                                                                                    UNIPROT: Q9LNC6; UNIPARC: UPI00000AC01F; GB: AE005172; NID: g8844126;
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                          90.2%;
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Score
Pred.
2; Mis
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Pred.
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Pred. No. 20;
ced. No. 94;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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C;Species: Homo sapiens (man)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-J
C;Accession: A43817
R;Blake, T.J.; Shapiro, M.; Morse III, H.C.; Langdon, W.Y.
Oncogene 6, 653-657, 1991
A;Title: The sequences of the human and mouse c-cbl proto-oncogenes A;Reference number: A43817; MUID:91232862; PMID:2030914
A;Accession: A43817
guanylate cyclase (EC 4.6.1.2) 2D-like precursor, 1
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996
C;Accession: I59385
R;Lowe, D.G.; Dizhoor, A.M.: Idn. K. C. C
                                                                                                                                               RESULT 13
I59385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-1103 <GOR>
A;Cross-references: UNIPROT:002740; UNIPARC:UPI0000128C1F; GB:U95958; NID:g2072999; PII
A;Experimental source: retina
C;Comment: This enzyme belongs to the subfamily of calcium-modulated rod outer segment
C;Superfamily: membrane-bound guanylate cyclase; guanylate cyclase catalytic domain hom
C;Keywords: phosphorus-oxygen lyase
C;Keywords: phosphorus-oxygen lyase
F;11-50/Domain: signal sequence #status predicted <SIG>
F;51-465/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Goraczniak, R.; Duda, T.; Sharma, R.K.
Biochem. Biophys. Res. Commun. 234, 666-670, 1997
A;Title: Structural and functional characterization of a
A;Reference number: JC5581; MUID:9731835; PMID:9175772
A;Accession: JC5581
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             guanylate cyclase (EC 4.6.1.2) ROS-GC2 precursor - bovine N;Alternate names: quanyl cyclase: cmanyly cyclase:
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C;Keywords: DNA binding
F;377-425/Domain: RING finger homology <RRNs
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F;1099-1103/Region: signature
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A; Residues: 1-906 <BLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;466-490/Domain: transmembrane #status predicted <TRM>
;523-816/Domain: protein kinase homology <KIN>
;836-1064/Domain: guanylate cyclase catalytic domain homology
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Pred. No. 2.3e+02;
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Pred. No. 2.9e+02;
2; Mismatches 0
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     Q.; Spencer, M.; Laura, R.; Lu, L.;
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                                                                                                                                      R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70977
                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein Rv3447c - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Decies: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004 C;Accession: E70977
                                                              A; Molecule type: DNA
A; Residues: 1-1236 <COL>
           A; Experimental source:
                                  A; Cross-references:
                                                                                                               A; Status: preliminary; nucleic acid sequence not shown; translation not
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UNIPROT: 006264; UNIPARC: UPI00000C150F; GB: Z95389; GB: AL123456;

NID

complete

genome

Holroyd, Gordon,

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strain

H37Rv

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C;Accession: B55915, R;Yang, R.B.; Poster, D.C.; Garbers, D.L.; Fuelle, H.J. Proc. Natl. Acad. Sci. U.S.A. 92, 602-606, 1995 A;Title: Two membrane forms of guanylyl cyclase found in the A;Reference number: A55915; MUID:95132648; PMID:7831337 A;Accession: B55915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           guanylate cyclase
C;Species: Rattus
C;Date: 23-Mar-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: membrane-bound guanylate cyclase; guanylate cyclase c;Keywords: cGMP biosynthesis; glycoprotein; bhosphorus-oxygen lyase F;523-816/Domain: protein kinase homology <KIN> F;836-1064/Domain: guanylate cyclase catalytic domain homology <GCC
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A;Molecule type: mRNA
A;Residues: 1-1108 <RES>
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A; Cross-references: GDB: 701610
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A;Title: Cloning and expression of a second photoreceptor-specific membrane retina
A;Reference number: 159385; MUID:95298345; PMID:7777544
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A; Residues: 1-1108 < YAN>
                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
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용 성 Search completed: April 4, 2006, 13:17:26 Job time: 2.14529 secs C;Genetics: A;Gene: Rv3447c Query Match 90.2%; Score 37; DB 2; Length 1236; Best Local Similarity 71.4%; Pred. No. 3.2e+02; Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0; 1 RPLPIPP 7 ||:|:|| 1207 RPMPLPP 1213

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2: uniprot_trembl:*
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1 RPLPIPP 7
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Q8QRS6 HPV26
Q91755 HPV26
Q91755 HV26
Q91755 TRUMAN
Q93276 TREDE
RAGE BOVIN
Q62974 ORYSA
Q1051 LEIMA
Q4QUS1 SYMTH
Q81HMO PLAF7
Q67R30 SYMTH
Q81HMO PLAF7
Q67R30 SYMTH
Q7U7P1 SYMPX
Q82146 STRAM
Q568P5 BRARE
Q4P1B6 USTMA
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Q56UC1 ECOLI
Q47088 ECOLI
Q41D33 G1BZE
Q8FQU9 COREF
Q8J1Y5 ASHGO
Q6KU24 XENLA
PHK_STRAW
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25-OCT-2004 (TrEMBLrel. 2
25-OCT-2004 (TrEMBLrel. 2
25-OCT-2004 (TrEMBLrel. 2
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Hypothetical protein.
Escherichia coli.
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11_ECOLI

056UC1_ECOLI PRELIMINARY;

056UC1;
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STRAIN=MBU. E 412;
PubMed=15748977;
                                                                                   Escherichia coli.
                                                                                                               Name=cdtA;
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Q19 <u>2</u> 61	Q19261 CAEEL	N	312	90.2	37	IJ
Q5tp55	Q5TP55 ANOGA	N	176	90.2	37	4
Q88c27	Q88C27_PSEPK	N	161	90.2	37	ω
Q72j63	Q72J63_THET2	N	117	90.2	37	N
Q5sit2	Q5SIT2 THET8	N	117	90.2	37	_
P26548	VE4_HPV51	۲	87	90.2	37	0
Q4syk6	Q4SYK6_TETNG	N	3855	92.7	38	9
P22316	CAC1S_CYPCA	_	1852	92.7	38	8
Q6rkb0	Q6RKB0_BRARE	N	1847	92.7	38	7
9	Q9GRZ3 CAEEL	N	1641	92.7	38	9
Q93564	Q93564_CAEEL	N	1243	92.7	38	5
P22682	CBL_MOUSE	_	913	92.7	38	4.
Q98ty6	Q98TY6_CHICK	N	903	92.7	38	ω
Q61dm	Q61DM6_CAEBR	N	810	92.7	38	Ν

ALIGNMENTS

Total S., Cloomi M., Oswald E.; The Total S., Cloomi M., Oswald E.; RT diarrheagenic Escherichia coli isolates from 1 RL Res. Microbiol. 156:137-144(2005). DR EMBL; AF373206; AA765834.2; -; Genomic DNA. DR GO; GO:0009279; C:outer membrane (sensu Gram-n DR GO; GO:0009405; P:pathogenesis; IEA. DR InterPro; IPR003558; CDtoxinA. DR InterPro; IPR003752; Ricin B lectin. DR Ffam; PF03498; CDtoxinA; 1. NR PFANTS; PR01387; CDTOXINA. R PRINTS; PR01387; CDTOXINA. R PROSITE; PS01231; RICIN B LECTIN; 1. NH Hypothetical protein. SEQUENCE 224 AA; 24123 MM. Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia. NCBI_TaxID=562; Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia. 100.0%; Created) Last sequence Last annotation type IV 0 Created) Last sequence update) Last annotation update) Score 41; DB 2; Pred. No. 1.1e+02; ; Mismatches 0; 347CE412AEB95961 CRC64; PRT; PRT; sequence update) annotation updat IV subunit A. 237 224 from h Gram-negative Bacteria); IEA Ą ₿ update) n locus humans Length 224; Indels cdtB among in Iran."; <u>,,</u> Gaps 0

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Q4 OAC BAG OAC
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Q4ID33;
13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Hypothetical protein.
ORFNames=FG04875.1;
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NUCLEOTIDE (
STRAIN=28C;
Ledger N., |
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EMBL; AY578329; AAT92047.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and sequencing of the genes encocytolethal distending toxin ";
Infect. Immun. 62:244-251(1994).
EMBL; U03293; AAD10621.1; -; Genomic_DNA.
GO; GO:0009279; C:outer membrane (sensu GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
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MEDLINE=94086109; PubMed=8262635;
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NCBI_TaxID=562;
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Q47088;
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                                 Gibberella zeae PH-1.
Eukaryota; Fungi; Ascomycota;
Hypocreomycetidae; Hypocreale
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PRINTS; PR01387; CDTOXITA.
PROSTTE, PS50231; RICIN B LEC-
SEQUENCE 237 AA; 25596 MW;
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InterPro; IPR000772; Ricin_B_lectin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.B.;
                                        Hypocreales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25483 MW; 45C29A34455ECBDA CRC64;
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25596 MW; 6D7
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Last annotation updat
                                                                                                                                                                                                                                                                 Created)
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Pred. No. 1.2e+02;
                                        Pezizomycotina;
s; Nectriaceae; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6D7EC323E4968E4E CRC64;
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RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkly L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Erickson J., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Hagopian D., Hagos R., Jones C., Kamal M., Kamata A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Male C., Johnson R., Jones C., Kamal M., Kamata A., Karatas A.,
RA Male D., Johnson R., Jones C., Macdonald P., Major J., Manning J.,
RA Matthews C., Manceli E., McCarthy M., Meldrim J., Meneus L.,
RA Minova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Matthews C., Mangae V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA Mandams J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkatazaman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Mu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches 7
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Q8FQU9;
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01-MAR-2004 (7
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"Fusarium graminearum genome sequence.";

Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases

Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases

-i- CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren
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EMBL; BA000035; BAC17828.1; -; Genomic_DNA HSSP; P36649; 1N68.
GO; GO:0005507; F:copper ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; InterPro; IPR011706; Cu-oxidase 2. InterPro; IPR011707; Cu-oxidase 3.
                                                                                                                                                                                                                                                                                                            STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium efficiens.
Bacteria, Actinobacteria; Actinobacteridae; Actinomycet
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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                                                                                                                                                                               replacements efficiens.";
                                                                                                                                                                                                                                                                            Sugimoto S.,
                                                                                                                                                                                                                                                                                  Nishio Y., Nakamura Y., Sugimoto S., Matsui K.,
                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=152794;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Putative oxidase.
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SEQUENCE 506 AA; 5
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                                                                                                                                                          Genome Res.
                                                                                                                                                                                                                                                               Gojobori T.,
                                                                                                                                                                                                                               "Comparative
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(TrEMBLrel.
                                                                                                                                                          13:1572-1579(2003).
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ble for the thermostability of Corynebacterium
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                                                                                                                                                                                                                                                                                  Kawarabayasi
Yamagishi A.,
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                                                  activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
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RESULT 7
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Pfam; PF07731; Cu-oxidase 2; 1.
Pfam; PF07732; Cu-oxidase 3; 1.
TIGRFAMS; TIGR01409; TAT signal seq; 1.
PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
                                     05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                        EMBL;
                                                                    Q6NU24 XENLA
Q6NU24;
                                                                                                                                                                                                                                                                                                                                                 Walther A., Wendland J.;
"Apical localization of actin patches and gossypii depend on the WASP homolog Wallp.
J. Cell Sci. 117:4947-4958(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2004 (TrEMBLrel. 26,
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata;
 Eukaryota; Metazoa;
                    Name=MGC81305;
                               MGC81305 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_
                                                                                                                                                                                                                                                                                                                                                                                                                      Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacc
Saccharomycetales; Saccharomycetaceae; Eremothecium.
NCBI_TaxID=33169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=WAL1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBJ1Y5_ASHGO
QBJ1Y5;
                                                                                                                                                                                                                                                                                                            Submitted (AUG-2002)
                                                                                                                                                                                                                                                                                                                       Wendland J.W.,
                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                         PubMed=15367585;
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IPR011993; PH type.
IPR001960; WHI.
IPR003124; WH2_actin_bd.
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IPR006311;
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Pred. No. 4e+
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                                                                                                                         Query Match
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Matches
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A Klein S., Strausberg R.;

Submitted (ARR-2004) to the EMBL/GenBank/DDBJ databases.

C. -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein

C. -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

R EMBL; BC068778; AAH68778.1; -; mRNA.

R GO; GO:0004524; F:ATP binding; IEA.

R GO; GO:0004474; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

R GO; GO:0004648; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006471; Ser thr pkin AS.

InterPro; IPR008271; Ser thr pkin AS.

InterPro; IPR002290; Ser thr pkinase.

InterPro; IPR002290; Ser thr pkinase.

InterPro; IPR002290; Ser thr pkinase.
                                                                                                                                                                                                                                                                             ProDom; PD000001; Prot kinase; 1.

SMART; SM00220; S TKC; 1.

SMART; SM00220; TyrKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE TT; 1.

PROSITE; PS00108; PROTEIN KINASE TT; 1.

PROSITE; PS00108; PROTEIN KINASE TT; 1.

PROSITE; PS00108; PROTEIN KINASE TT; 1.

SETINE/threonine-protein kinase; Transferase.
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Proc. Natl. Acad. Sci. U.S.A.
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Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00069; Pkinase;
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Klein S.L., Strausberg R.L., Wagner
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   RPLPIPP
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Pred. No.
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RESULT 9
Q8Q941 9BETA PRELIMINARY;
ID Q8Q941;
AC Q8Q941;
DT 01-JUN-2002 (TrEMBLrel. 21, C:
DT 01-JUN-2003 (TrEMBLrel. 23, L:
DT 01-MAR-2003 (TREMBLrel. 23, L:
DT 01-MAR-2003 (TREMBLrel. 23, L:
DE Tegument protein UL48.
OS Pongine herpesvirus 4 (Chimpa:
OC Viruses; dsDNA viruses, no RN;
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STRAIN-MA-4680 / ATCC 31267 / NCIMB 12804 / NRIL 8165;
MEDLINE=21477403; PubMedel1572948; DOI=10.1073/pnas.211433198;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Office Conveyors avermitilis.
Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Bacteria; Actinobacteria; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence and comparative analysis microorganism Streptomyces avermitilis."; Nat. Biotechnol. 21:526-531(2003).
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STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;
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10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Probable phosphoketolase (EC 4.1.2.-).
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10-MAY-2005
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Sakaki Y., Hattori M., Omura S.;
Tegument protein UL48.
Pongine herpesvirus 4 (Chimpanzee cytomegalovirus)
Viruses; dsDNA viruses, no RNA stage; Herpesvirida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAP; MF 01403; -; 1.
InterPro; IPR012109; Phosphoketolase.
InterPro; IPR000399; TPP_bd.
InterPro; IPR005593; XFP.
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Pred. No. 4.4e+02;
Mismatches 0;
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RESULT 10
Q5VPS2 ORYSA
ID VG5VPS2;
AC Q5VPS2;
DT 01-FEB-2005 (TrEMBLrel. 29,
DE Nucleoid DNA-binding protein
GN Name-OSJNBa0062J13.18;
OS Oryza sativa (japonica cult:
OC Eukaryota; Viridiplantae; SI
OC Spermatophyta; Magnoliophyt:
OC Ehrhartoideae; Oryzeae; Ory:
OX NCBI_TaxID-3947;
RN NCCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yal
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yal
RT clone:OSJNBa0062J13.";
RL Submitted (MAY-2001) to the
DR GO; GO:0003577; F:DNA bindi
KW DNA-binding.
SQ SEQUENCE 175 AA; 18553 M
                                                                                                                                                                                                                                                                                                                               RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Oryza sativa nipponbare(GA3) genomic DNA, chrom clone:OSJNBa0062J13:";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ day
EMBL, AP003564; BAD68553.1; -; Genomic DNA.
GG; GO:0003677; F:DNA binding; IEA.
DNA-binding.
DNA-binding.
SEQUENCE 175 AA; 18553 MW: Coccommodity
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Best Local S
Matches 7
                                                                                                                    .X2_HUMAN STANDARD; PRT; 284 AA.

TIX2 HUMAN STANDARD; PRT; 284 AA.

043763; Q9UQ48;

15-JUL-1999 (Rel. 38, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

10-MAY-2005 (Rel. 47, Last annotation update)

10-MAY-2005 (Rel. 47, Last annotation update)

T-cell leukemia homeobox protein 2 (Homeobox protein).

Name=TIX2; Synonyms=HOX11L1, NCX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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NUCLEOTIDE SEQUENCE.

MEDLINE=22421467; PubMed=12533697; DOI=10.1099/vir.0.18606-0; MEDLINE=22421467; PubMed=12533697; DOI=10.1099/vir.0.18606-0; Davison A.J., Dolan A., Akter P., Addison C., Dargan D.J., Alcendor D.J., McGeoch D.J., Hayward G.S.;

"The human cytcomegalovirus genome revisited: comparison with the chimpanzee cytcomegalovirus genome."; Chimpanzee cytcomegalovirus genome.";

J. Gen. Virol. 84:17-28(2003).

J. Gen. Virol. 84:17-28(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation updat
Nucleoid DNA-binding protein cnd41-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Betaherpesvirinae;
NCBI_TaxID=188763;
                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                     Homo sapiens (Human)
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity nes 7; Conserv
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                                                 Chordata; Craniata; Vertebrata;
Euarchontoglires; Primates; Cata
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85.7%;
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Pred. No. 1.2e+02;
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Pred. No.
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[1]
NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
Delgado P., Rodriguez R.E., Gonzalez-Sarmiento R.;
"Genomic characterization and chromosomal location homeobox gene HOX1111.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ datal
 Developmental
DNA BIND 15
COMPBIAS 2
CONFLICT 1
CONFLICT 3
CONFLICT 1
CONFLICT 1
CONFLICT 1
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CONFLICT 1
CONFLICT 1
                                                                 PROSITE; PS00027; HOMEOBOX 1; 1.

PROSITE; PS00027; HOMEOBOX 2; 1.

PROSITE; PS50071; HOMEOBOX 2; 1.

PROSITE; PS50071; HOMEOBOX 2; 1.

"DNA-binding; Unamobo
                                                                                                                                                                      MIM;
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EMBL; AJ002608; CAA05636.1; JOINED; Genomic_DNA.
EMBL; AJ002609; CAA05636.1; JOINED; Genomic_DNA.
EMBL; AB008501; BAA05631; -; mRNA.
EMBL; BC006356; AAH06356.1; -; mRNA.
HSSP; P13297; IIG7.
                                                                                                                                                                                                                                                                                                        This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99377083; PubMed=10446220; I

litsuka Y., Shimizu H., Kang M.M., S

Tokuhisa T., Hatano M.;

"An enhancer element for expression

neural crest-derived cells.";
                                                                                                     Pfam; PF00046; Homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                              HGNC;
                                                                                                                                                                                      Ensembl; ENSG00000115297;
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                                                                                                                                                                                                                                                                                                  use as
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                                                                                                                                              InterPro; IPR001356; Homeobox.
InterPro; IPR012287; Homeodoma
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al protein;
157 216
27 116
16 16
30 32
37 48
100 102
131 136
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Gly-rich.
P -> A (in Ref. 1).
TPG -> PR (in Ref. 1).
IGRGGQGHGENG -> WVAGQVIGEWA (
Missing (in Ref. 1).
RLTAAL -> PAV (in Ref. 1).
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Sasagawa K., Sekiya S.,
                                                                         Homeobox; Nuclear
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TLX2_MOUSE
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Matches 6
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CONFLICT
                                                                                                                                                                                                                                                                                                                       10q24.";
Proc. Natl. Acad. Sci. U.S.A. 88:8900-8904(1991).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: Contains 1 homeobox DNA-binding domain.
-!- CAUTION: Was originally (Ref.1) thought to be the ortholog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1-cell leukemia homeobox protein 2 (Homeobox
                                                                                                                                        Ensembl; ENSMUSG00000030040; Mus musc
MGI; MGI:1350935; Tlx2.
InterPro; IPR001356; Homeobox.
InterPro; IPR012287; Homeodomain-rel.
Pfam; PF00046; Homeobox; 1.
                                                                                    PRODOM; PD000010; Homeobox; 1.
SMART; SM00389; HOX; HOMEOBOX 1; 1.
PROSITE; PS00027; HOMEOBOX 2; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                    Kennedy M.A., Gonzalez-Sarmiento R., Boehm T., Rabbitts T.H.; "HOX11, a homeobox-containing T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Euarchontoglires; G
Muroidea; Muridae; Murinae; Mus.
                                                       COMPBIAS
                                                                   DNA BIND
                                                                            Developmental
                                                                                                                                                                                                                                 EMBL; M75953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Homeobox TLX-2) (PMUR10F).
Name=Tlx2; Synonyms=Hox1111,
Mus musculus (Mouse).
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                                                                                                                                PRINTS; PR00024; HOMEOBOX.
                                                                                                                                                                                                 TRANSFAC;
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                                                                                                                                                                                                                                                      removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                    al protein; DNA-binding; Homeobox; Nuclear 157 216 Homeobox.
                                             284 AA;
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   Conservative
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           Score 40;
Pred. No.
                                    Gly-rich.
; CD1D6D3EB0F8CBDA CRC64;
Pred. No. 2.1
1; Mismatches
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V -> A ()
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            Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                      outstation
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RESULT 13

Q8QRS5 9BETA

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DE Transcri

OS Pongine

OC Viruses

OC NCBI_TS

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RT chimpana

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DR InterPcc

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                  A Altern B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E., An Altern B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E., An Altern B., Nusbaum C., Allen T., An P., Anderson M., Anderson S., An Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S., An Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A., An Arachchi H., Armbruster B., Bloom T., Blye J., Boguslavskiy L., Ra Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N., An Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N., Cooke P., Corum B., Cuomo C., Ra Borowsky M., Boukhgalter B., Brunache A., Cooke P., Corum B., Cuomo C., Ra Dorjee K., Dorris L., Campo K., Cooke P., Corum B., Cuomo C., Ra David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P., Ra Dorjee K., Dorris L., Duffey N., Duges A., Elkins T., Engels R., Ra Dorjee K., Dorris L., Duffey N., Duges A., Elkins T., Engels R., Ra Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S., Ra Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S., Ra Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H., Ra Hagopian D., Hagos B., Hall J., Hatcher B., Hume W., Husby E., Iliev I., Ra Hagopian D., Jones C., Kamal M., Kamat A., Kamvysselis M., Karlsson E., Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K., Ra Lindblad-toh K., Liu X., Nabbitt R., Macdonald J., Maclean C., Major J., Ra Lui A., Ma L.J., Mabbitt R., Maru K., Matthews C., Mauceli E.,
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Best Local :
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01-JUN-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Transcriptional transactivator TRS1.
Pongine herpesvirus 4 (Chimpanzee cytomegalovirus).
Viruses, dsDNA viruses, no RNA stage, Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      i3-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 113-SEP-2005 (TrEMBLrel. 31, Hypothetical protein. ORFNames=UM00873.1;
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MEDILINE=22421467; PubMed=12533697; DOI=10.1099/vir.0.18606-0;

MEDILINE=23421467; PubMed=12533697; DOI=10.1099/vir.0.18606-0;

Davison A.J., Dolan A., Akter P., Addison C., Dargan D.J.,

Alcendor D.J., McGeoch D.J., Hayward G.S.;

"The human cytomegalovirus genome revisited: comparison with the
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J. Gen. Virol. 84:17-28(2003).
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NCBI_TaxID=188763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes; Ustilaginomycetidae; Ustilaginales; Ustilaginaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003360; US22. Pfam; PF02393; US22; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=237631;
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85.7%;
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Last annotation updat
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Pred. No. 6.8e+02;
1; Mismatches 0
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Iliev I.,
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RESULT
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Matches 6
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13Z6 HPV26
Q993Z6_HPV26 PRELIMINARY
Q993Z6;
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
Putative E4 protein.
Putative E4 protein.
Human papillomavirus - 81
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Terai M., Burk R.D.;

Submitted (AUG-2000) to the EMBL
EMBL; AP293961; AAK28453.1; -; G
InterFro; IPR003861; Pap.110ma_E
Pfam; PF02711; Pap_E4; 1.

SEQUENCE 88 AA; 10084 MW; 67
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Alphapapillomavirus.
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1 (TrEMBLrel. 17,
4 (TrEMBLrel. 26,
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Pred. No. 8.7e+02;
                                                                                                                                                                                Score 39; DB
Pred. No. 85;
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D., Yadav S.,
un J., Zembeck L.,
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Tchuinga P.,
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Search completed: April Job time: 8.35079 secs

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Perfect score:
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	_		CAP6	Human pro	Human hea	PI3 kinas	Human	Human	Human pro	Rat	Rat	3	Bacteria]	Novel hur	Rice abic	Novel	Pseudomor	Human	Novel	Streptocc

ALIGNMENTS

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XX Modi
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XX W Inh
PD 04-i
XX W IN
PF 25-i
XX C1
PR 23-i
P Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IT.; TNF; antiagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; 23-OCT-1998; 22-OCT-1999; 04-MAY-2000 AAB17234 standard; peptide; 7 AA. Feige U, (AMGE-) AMGEN INC. 25-OCT-1999; WO200024782-A2 Synthetic. thrombosis; pharmaceutical. SH3 antagonist 31-OCT-2000 Liu C, (first entry) 98US-0105371P 99US-00428082 peptide sequence SEQ 99WO-US025044 Cheetham Ç Boone ID NO:290. TC;

WPI; 2000-350702/30.

Aau48480 Abm44999

Novel composition of matter comprising an Fc active peptides, useful for treating cancer a c domain and pharmacologically and autoimmune diseases.

Claim 39; Page 298; 608pp; English.

100.0 100.0 100.0 92.3 92.3 92.3 92.3 92.3

ABB73228 ADJ73382 ADJ53016 ADJ51977 AAW11116 AAW25498 AAW16935 ABO77807

ABG07608 AAW72022 AAB17235 AAU50101 ABM46620 AAU48480 ABM44999 AAW16936 AAW25499

Aau50101 Abgu46620 Abgu7602 Abaw72022 Aab73235 Abb73235 Abb73382 Adj73382 Adj53016 Ady151977 Aaw151977 Aaw25498

Random Random

antag delet delet SH3 d dom pe

100.0 100

The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where FI = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,

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RRESULT 2
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ID ABB73227
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KW MMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TWP-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP; TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antiinfeammatory; antituto; antidabetic; ophthalmological; antianaemic; anorectic; antiinfertility; haemostatic; dermatological; antianaemic; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; anaemia; thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
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     multimers. (I) can have an cytostatic, antirheumatic, antianaemic, anorectic, an
                                                                                                                                                                                                     Novel vehicle-peptide molecule inflammatory and autoimmune dis diabetic retinopathy, obesity,
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                                                                                                                                                     Claim
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     present invention describes a vehicle-peptide molecule (I) or its timers. (I) can have antiinflammatory, antitumour, immunosuppressive, ostatic, antirheumatic, antiarthritic, antidabetic, ophthalmological ostatic, anorectic, antiinfertility, haemostatic, dermatological and
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Pred. No. 2e+
D; Mismatches
                                                                                                                                                                                                                                      or its multimers useful for treating seases, cancer, rheumatoid arthritis,
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Best Local (
                                                                                                                                                              New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region, useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mimetic; CDR mimetibody; gene therapy; transgenic; immune;
cardiovascular; infectious; malignant; neurologic disease; anaemia;
immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunomodulator;
                                                                                                                                                                                                                                                                                                                                                           (CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                      2003-804237/75
                                                                                                                                                                                                                                                                                                                 GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPLPSRP
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                                                                                                                                                                                                                                                                                                                    Ghrayeb J;
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This invention relates to novel mammalian CDR mimetibodies, specific portions or variants thereof. Specifically, it refers to an antibody fragment where a protein has been inserted into, or replaces a portion of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which

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RESULT 4
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This invention relates to CH1 deleted mimetibodies (and the DNA sequence which encode them), compositions, methods and uses. The invention may be useful for the development of compounds with an immunosuppressive, cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, antibacterial, virucide or fungicide activity. In addition, the discloss sequences may prove useful for gene therapy. The CH1-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell,
                                                                                                                                                                                                                                                                                                                          New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, or neurodegenerative disease or disorder, anemia, cancer, or infectious
                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUN-2002; 2002US-0392431P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUN-2003; 2003WO-US020347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hypertension; heart failure; neurodegenerative; multiple solerosis; dementia; Alpheimer's disease; anaemia; cancerous condition; infectious disease; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CH1 deleted mimetibody-related peptide SeqID836.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kutoloski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heavner GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypotensive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  2004-082870/08
                                                                                                                                                                                                                                         3; SEQ
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                                                                                                                                                                                                                                      NO 836; 129pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fungal infection.
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Pred. No.
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2e+06;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder; dental disorder; oral disorder; dermatological disorder; ear disorder; nose disorder; throat disorder; endocrine disorder; metabolic disorder; gastrointestinal disorder; gynaecological disorder; hepatic disorder; gobstetric disorder; haematologic disorder; immunological disorder; altergic disorder; infectious disorder; immunological disorder; oncological disorder; neurological disorder; nutritional disorder; ophthalmologic disorder; pediatric disorder; psychiatric disorder; pulmonary disorder; psychiatric disorder; pulmonary disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue, organ or animal, specifically for modulating, treating, alleviating, preventing the incidence or reducing the symptoms of an immune, cardiovascular (for example arrhythmia, hypertension or heart failure), or neurodegenerative (for example multiple sclerosis, dementia or Alzheimer's disease) diseases or disorders, anaemia, cancerous conditions, or infectious diseases (for example bacterial, viral or fungal infection). The present sequence is that of a peptide which may be used during the creation of a mimetibody of the invention.
                                                                          diagnosing, preventing, endocrine, gastrointestinal,
                                                                                     New CH1 deleted mimetibody polypeptide and nucleic acid, useful diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; gynaecological-Gen; hepatotropic; haemostatic; immunomodulator; antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;
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19-SEP-2002;
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                                                                                                                                                                                                                                   (CENZ ) CENTOCOR INC.
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KA;
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2002US-0412144P
                                                                                                                                                                                                   Knight
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Claim

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English.

invention relates to CH1 deleted mimetibodies h encode them), compositions, methods and uses.

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invention

DNA sequences ention may be

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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 7
                 AAW11098-W11124 are peptides that bind to the Src SH3 domain. The SH3 binding peptides are useful in modulating signal transduction pathways at the cellular level (especially protein tyrosine kinase-mediated), modulating oncogenic protein activity, or providing compounds for the development of drugs with the ability to modulate broad classes, as well as specific classes, of proteins involved in signal transduction and also for remulations of proteins involved in signal transduction and also
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                                                                                                                                                                                                                                                                                                                                            Peptide with binding affinity for Src homology region 3 (sproteins - useful for e.g. modulating signal transduction cellular level, esp. protein tyrosine kinase-mediated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-FEB-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-117151/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sparks
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                                                                                                                                                                                                                                                                        40; Page 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AΒ,
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7; Conserv
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95US-00483555.
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processing,
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Pred. No.
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                                                                              AAW16924-W16948 are random recombinant peptides derived from one of three peptide libraries, T9, T12 and R8C. The peptides are all SH3 domain-binding peptides. SH3 binding peptides are useful in modulating signal transduction pathways at the cellular level (especially protein tyrosine kinase-mediated), modulating oncogenic protein activity, or providing compounds for the development of drugs with the ability to modulate broad classes, as well as specific classes, of proteins involved in signal transduction and also for regulating the processing, trafficking or translation of RNA. Conjugates of the peptides with detectable labels or imaging agents are useful for imaging cells, tissues and organs in which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Src; SH3; Src homology region 3; binding affinity; oncogenic protein tyrosine kinase; signal transduction; RNA processing; trafficking; translation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conjugates of the peptides with detectable labels or imaging agents are useful for imaging cells, tissues and organs in which Src or Src-related
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                                                                                                                                                                                                                                             Peptide with binding affinity for Src homology region 3 (SH3) domains proteins - useful for e.g. modulating signal transduction pathways at cellular level, esp. protein tyrosine kinase-mediated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                        Src
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07-JUN-1995;
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95US-00483555
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           100.0%;
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Pred. No.
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Matches 7
                                                                                                                                                                       peptides are selected from: (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of Nck; (c) peptides which bind the SH3 domain of Nck; (d) peptides which bind the SH3 domain of Nck; (e) peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of Crk; (h) peptides which bind the SH3 domain of Grk; (r) peptides which bind the SH3 domain of Grk2. The purified binding peptides can be used in the method to identify inhibitors of their binding to their respective SH3 domains, which could be used to modulate the pharmacological activity of proteins or polypeptide containing the SH3 domain. The peptides can also be used to activate Src or Src-related protein tyrosine kinases, to stimulate the immune response by increasing the production of certain lymphokines, e.g. tumour necrosis factor-alpha and interleukin-1, or to deliver a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sparks AB,
Rider JE;
                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a random peptide recombinant isolated the method of the present invention. SH3 (Src homology region 3) bindi
                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 5; 131pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              certain lymphokine(s), e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Src homology region 3 binding peptide - used to activate Src tyrosine kinase(s) and to stimulate immune response by increasing production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cortactin; SH3 domain; binding peptide; Src homology region 3; tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl;
                                                                                                                                                               conjugated molecule to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-424972/39
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                           1 RPLPSRP 7
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                                                                                                                                                            certain cellular
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Pred. No.
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                                                                                                                                                            compartments containing Src or
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cc pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

Cc P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory comercial sasociated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The compression and activity of P. acnes proteins of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes paypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining. ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
Matches
                  Query Match
Best Local :
                                                                  Sequence 79
                                                                                                                                                                                                                                                                                                                                                                           Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes polypeptides and nucleic acids useful vaccinating against and diagnosing infections, especially usefureating acne vulgaris.
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02-JUN-2000; 2000US-0208841P
07-JUL-2000; 2000US-0216747P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; SEQ ID NO 9675; 1069pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dermatological; osteopathic; neuroprotectant.
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Similarity 7; Conserv
                                                                    AA;
100.0%; illarity 100.0%; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitcham JL, Wang SS,
, Jen S, Carter D;
 0
                  Score 39;
Pred. No.
 Mismatches
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                   59;
                                  DB 4;
 <u>,</u>
                              Length 79;
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ABM44999 standard; protein; 79

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CC encoding a Propionibacterium acnes protein. The invention also relates to CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to CC immunogenic fragments of P. acnes polypeptides. The invention also relates to CC additionally encompasses expression vectors and host cells comprising a CC polynucleotide of the invention; antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; antibodies against polypeptides of the comprising an immune response specific for a P. acnes cc method for stimulating an immune response specific for a P. acnes polypeptide, antibodies, fusion proteins; T cell populations, or CC polynucleotides, antibodies, fusion proteins; T cell populations, or CC patient. The P. acnes polypeptides, polynucleotides, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptide; a method and kit for detecting or determining the presence or absence of P. acnes in a CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for inhibiting the development of P. acnes in a CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for dargnosing, preventing or treating acne composition. The polynucleotides can also be used as probes or primers for CC conditions of an immune response specific for a P. acnes for cc patient of the vaccine composition is useful for the cc and the kit is useful for performing a diagnostic assay. The present cc invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences
                                                                                                                                            Query Match
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Zhang Y, Wa
Barth B, Va
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 9675; 1481pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes predicted ORF-encoded polypeptide #9675
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                                                                    RPLPSRP 7
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                                                                                                                                            Conservative
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                                                                                                                                            100.0%; Score 39; DB
100.0%; Pred. No. 59;
tive 0; Mismatches
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Benson DR,
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Jones R, Carte
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                                                                                                                                                                                                                 polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central pervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to compregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was completed by the protein in electronic format directly from WIPO at
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02-JUN-2000; 2000US-0208841P
07-JUL-2000; 2000US-0216747P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes vaccinating against and treating acne vulgaris.
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                                                                                                                             Sequence
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DB; AAS59546.
   l Similarity
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         Conservative
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         100.0%; Score 39; DB
100.0%; Pred. No. 63;
tive 0; Mismatches
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, Jen S, Carter
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arter D;
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RESULT 12
ABM46620
                                                                                                              cc encoding a Propionibacterium acnes protein. The invention also relates to Cc polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to Cc immunogenic fragments of P. acnes polypeptides. The invention of composent fragments of p. acnes polypeptides. The invention of the invention; antibodies against polypeptides of the invention; antibodies against polypeptides of the invention; a method for stimulating an immune response specific for a P. acnes cc method for stimulating an immune response specific for a P. acnes polypeptides, antibodies, fusion proteins, T cell populations, or cc antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a cc patient; and a method for inhibiting the development of P. acnes in a cc patient. The P. acnes polypeptides, polynucleotides, antibodies, tusion proteins, T cell populations or antigen-presenting cells that express the polypeptides, antibodies in a cc patient. The P. acnes polypeptides, polynucleotides, antibodies the complexity or for stimulating an immune response specific for a P. acnes complexity. The polynucleotides can also be used as probes or primers for complexity or far stimulating an immune response specific for a P. acnes composition is useful for the complexity of the primers for conclete acid hybridisation. The vaccine composition is useful for the complexity of the primers for conclete acid hybridisation. The vaccine composition is useful for the complexity of the primers for conclete acid hybridisation and the P. acnes polypeptide by an order the complexity of the present conclete acid hybridisation, but was obtained in electronic format directly contained within the P. acnes polypucleotides of the complexity of the primers for the primers for the primers for the primers of the complexity of the primers for the primers of the complexity of the primers for the primers of the complexity of the primers for the primers for the primers for the primers for the primer
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Zhang Y,
Barth B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-OCT-2003
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h 100.0%;
Similarity 100.0%;
7; Conservative 0;
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Wang S, Jen S, Lodes MJ,
Vallieve-Douglass J;
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Score 39; DB Pred. No. 63; 0; Mismatches
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Benson DR,
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Jones R, Carter D;
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RESULT 13
ABG07608
                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) consequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used to in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cuseful for generating antibodies against it, detecting or quantitating a colypeptide in tissue, as molecular weight markers and as a food conjugation of the binding partners are useful in medical imaging consists expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The colypeptide and polynucleotide sequences have applications in conjugation, forensics, gene mapping, identification of mutations crasponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cannot acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences in the printed specification, but was obtained in celectronic format directly from WIPO at fig., wipo.int/pub/published_pct_sequences
Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                     Sequence 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID NO 37967; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS71795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #7599
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100.0%;
ilarity 100.0%;
Conservative 0
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      Score 39; DB 4;
Pred. No. 1.4e+02;
; Mismatches 0;
                                                                     Length 199;
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RESULT 14
AAW72022
ID AAW77
RESULT 15
AAB17235
ID AAB17
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AC AAB17
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DT 31-OC
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Matches 7
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Leary JJ;
                                                                                                                                                                                                                                                                                                                                       This sequence represents a Herpes simplex virus type-2 (HSV-2) protein sequence of the invention. This sequence was isolated from a HSV-2 straises (deposited as ATCC VR-2546) DNA fragment designated Contig ID 102. The proteins can be used for the treatment or prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Antagonists of the proteins can be used to inhibit a viral polypeptide. The DNA sequence or a vector containing it can also be used to induce an immunological response in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herpes simplex virus type-2 sequences - useful in, e.g. prevention and treatment of infection or inducing immunological response in mammal.
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09-JUN-1997;
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                                                                                                                                                                                                                                                                                                                  Sequence 351 AA;
    Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VE
                                                                                                                                 AAB17235 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 47; 748pp; English.
                                              SH3 antagonist peptide sequence SEQ ID NO:291.
                                                                          31-OCT-2000
                                                                                                      AAB17235;
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                                                                                                                                                                                                                                                            Similarity 7; Conserv
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97US-0049018P.
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                                                                                                                                                                                                                                                          Score 39; DB 2;
Pred. No. 2.3e+02;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                      Length 351;
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Search completed: April Job time : 4.47251 secs
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                                                                                                                                                                                                                                                                                                                                             The present invention describes composition of matter (I) comprising an CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is: CC (XI)a-FI-(XZ)b, where: FI = an Fc domain; XI and XZ = are each CC (II)d-P2-(IJ)e-P3-(I)e-P3-(II)c-P1-(IL)c-P1-(IL)c-P1-(IL)d-P2, -(IL)c-P1-(IL)d-P2, -(IL)c-P1-(IL)c-P1-(IL)d-P2, -(IL)c-P1-(IL)d-P2, -(IL)d-P2, -(IL)d-P2, -(IL)c-P1-(IL)d-P2, -(IL)d-P2, -(IL)d-P2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
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22-OCT-1999;
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                                                                                                                                                                                                                                                                                                      Sequence 7
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                                                                                                                                                                                                      Similarity 6; Conserv
                                                                                                        RPLPTRP
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99US-00428082.
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85.7%;
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Pred. No. 2e+06;
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Result
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Maximum DB
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Perfect score:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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A72594
G87498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gag-pro-pol polyprotein - walleye dermal sarcoma virus
C;Species: walleye dermal sarcoma virus
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T09394; T09393
R;Petropoulos, C.J.
submitted to the EMBL Data Library, November 1997
A;Description: Appendix 2: Retroviral taxonomy, protein structure, sequences, and gene A;Reference number: Z16660
A;Accession: T09394
A;Status: translated from GB/EMBL/DDBJ
A;Cross-references: UNIPROT:092815; UNIPARC:UPI000010BDA0; EMBL:AF033822; NID:g2801519
A;Cross-references: UNIPROT:092815; UNIPARC:UPI000010BDA0; EMBL:AF033822; NID:g2801519
A;Molecule type: genomic RNA
A;Residues: translated from GB/EMBL/DDBJ
A;Molecule type: genomic RNA
A;Residues: 1-1582 <PEW>
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45	44	4.	42	41	40	39	38	37	36	35	34	33	32	31	30
33	ω ω	ω ω	ω	33	33	33	33	33	33	33	33	33	33	34	34
84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	87.2	87.2
459	451	432	348	317	314	278	233	227	196	85	85	82	75	1611	1440
N	N	N	N	N	N	μ.	N	N	N	N	N	N	N	N	N
S33000	B81850	A25483	T33179	E86264	T03775	TPHUTW	D95877	B83505	176912	S10119	S10120	C48349	S05589	T38236	T27942
hypothetical	exonuclease	env polyprotein	hypothetical	protein F3F19.7	DNA-binding homeot	troponin	probable	hypothetical prote	ychG protein	Balbiani	Balbiani	UL28 protein -	Balbiani	hypothetical	lin-15B protein -

ALIGNMENTS

RESULT 2 B87261 Bypothetical protein CC0099 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Accession: B87261 C;Accession: B87261 C;Accession: M.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, (Riterman, W.C.; Feldblyum, T.V.; Paulsen, J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kole, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.P. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001 A;Title: Complete Genome Sequence of Caulobacter crescentus. A;Reference number: A87249; MUID:21173698; PMID:11259647 A;Accession: B87261 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-103 <sto> A;Genetics: A;Genetics: A;Gene: CC0099</sto>	Query Match 100.0%; Score 39; DB 2; Length 1751; Best Local Similarity 100.0%; Pred. No. 77; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 RPLPSRP 7	A;Cross-references: UNIPARC:UPI000010499D; EMBL:AF033822; NID:g2801519; PID:g2801521 C;Genetics: A;Gene: gag-pro-pol A;Introns: 582/3

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transcription regulator, AraC family [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Species: Caulobacter crescentus C;Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Accession: C87568 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, R,Nierman, W.C.; Feldblyum, T.V.; Paulsen, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koll B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koll n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.N. proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001 A;Title: Complete Genome Sequence of Caulobacter crescentus.
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A;Notte: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AG1950
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG1950
RESULT 5
B38749
3-phosphatidylinositol kinase (EC
C;Species: Bos primigenius taurus
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A;Molecule type: DNA
A;Residues: 1-270 <STO>
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A; Residues: 1-369 < KUR>
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Pred. No. 40;
1; Mismatches
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Pred.
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        (cattle)
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AH2827
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; Karp, P.; Romero, P.; Zhang, Science 294, 2317-2323, 2001

A; Authors: Yoo, H.;

Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm

L.; Wood, G.E.; Chen, in, T.; Levy, R.; Li,

M.; McClel

Engineer Agrobacterium tumofaciens PMID:11743193

C58

Agrobacterium tumefaciens (strain C58,

A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; MUID:21608550;

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C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 15-Mar-2004 C;Accession: B38749 R;Otsu, M.; Hiles, I.; Gout, I.; Fry, M.J.; Ruiz-Larrea, F.; Panayotou, G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:000459; UNIPARC:UPI000013106C; GB:NP_005018; PID:g4826908; R;Janssen, J.W.; Schleithoff, L.; Bartram, C.R.; Schulz, A.S. Oncogene 16, 1767-1772, 1998
A;Title: An oncogenic fusion product of the phosphatidylinositol 3-kinase p85beta subur A;Reference number: A59436; MUID:98241181; PMID:9582025
A;Accession: A59436
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C;Keywords: phosphotransferase
F;325-420/Domain: SH2 homology <SH2A>
F;617-706/Domain: SH2 homology <SH2>
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A; Residues: 1-723 <OTS>
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A;Residues: 1-728 <JAN>
A;Cross-references: UNIPARC:UPI000013106C; GB:NP_005018; PID:g4826908;
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A; Accession: H59435
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A; Residues: 1-728 < JI
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A;Accession: AH2827
A;Status: preliminar
A;Molecule type: DNA
A;Residues: 1-175 <K
                                                                                                                                                                                                                     hypothetical protein 1 - Rhizobium meliloti (;Species: Rhizobium meliloti C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text C;Accession: $27657

R;Miller, K.J.; McKinstry, M.W.; Hunt, W.P.; Nixon, B. submitted to the EMBL Data Library, May 1992

A;Description: Identification of the diglyceride kinase A;Reference number: $27657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: circular cnro C; Superfamily: dihydrofolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dihydrofolate reductase (AP001518) [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 05-Oct-2004 C;Accession: F97605
C;Accession: F97605
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Go A.; Liù, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markel
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                                                                                                                                A;Molecule type: DNA
A;Residues: 1-208 <MIL>
A;Cross-references: UNIPROT:Q52921; UNIPARC:UPI00000B5865;
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A;Map position: circular chromosome
C;Superfamily: dihydrofolate reductase; type I dihydrofolate reductase
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C;Genetics:
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A; Residues: 1-175 < KUR>
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A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.; Liu, F.; Wollam, C.; Al.
Science 294, 2323-2328, 2001
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                                                                                 Similarity
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Pred. No. 45;
0; Mismatches
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Pred. No.
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Pred. No. 38;
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kelz, B.
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R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh DNA Res. 6, 83-101, 199
A;Title: Complete genome sequence of an aerobic hyper-thermophilic A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: F72561
                                                                                                         hypothetical protein APE1776 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: F72561
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C;Genetics:
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R;Vleek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkon
Proc. Natl. Acad. Sci. U.S. A. 94, 9384-9388, 1997
A;Title: Sequence of a 189-kb segment of the chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rhodobacter capsulatus
C;Date: 24-Mar_1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
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C;Superfamily:
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A; Residues: 1-240 <STO>
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A; Title: Complete genome s
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, 1; Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change
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                                                                                                                                                                                                      RESULT 12
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85.7%;
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                                                                     ; Haikawa, Y.
, T.; Kudoh,
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A;Molecule type: DNA
A;Residues: 1-127 <KAM'>
A;Residues: 1-127 <KAM'>
A;Cross-refrences: UNIPROT:Q9YB19; UNIPARC:UPI000005E0A7; DDBJ:AP000062; NID:g5105244;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1776
음 성
                                                                                                                                                                                                                                                          R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K. awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: F72470
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F72470
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A;Cross-references: UNIPROT:Q19751;
A;Experimental source: clone F23B12
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A;Reference number: Z19402
A;Accession: T21290
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T21290
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C;Becies: Aeropyrum pernix
C;Becies: Aeropyrum pernix
C;Bate: 20-Aug_1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: F72470
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                                                                                                                                       A;Gene:
                                                                                                                                                                    A;Cross-references: UNIPROT:Q9Y978; UNIPARC:UPI000005E32A; DDBJ:AP000064; NID:g5105945;
A;Experimental source: strain K1
                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-164 < KAW>
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C;Accession: F83305
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A:Reference number: A82950; MUID:20437337; PMID:10984043
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A;Residues: 1-179 <STO>
A;Cross-references: UNIPROT:Q9IOB8; UNIPARC:UPI00000C57D0; GB:AE004700; GB:AE004091; NI
A;Experimental source: strain PAO1
C;Genetics:
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Q59FE5 HUMAN
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Q55H6 THETS
Q9A584 CAUCR
Q5NTG0 9BACT
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Q72GL1 THETS
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Nocardia farcinobacteria; Actinobacteridae; Actinomycetales;
Bacteria; Actinobacteria; Occardia.
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Ishikawa J., Yamashita A., Mikami
Shiba T., Hattori M.;
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Pred. No. 2.9
0; Mismatches
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Pred. No.
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Y., Hoshino
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RESULT 5
Q5GXW8 y
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AC Q5GXW8;
DT 10-MAY-2
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Pfam; PF00078; RVT_11.
Pfam; PF00098; zf-CCHC; 1.
SMART; SM00343; ZnF C2HC; 1.
PROSITE; PS501879; RNASE H; 1.
PROSITE; PS50189; ZF CCHG; 1.
SEQUENCE 1751 AA; 196152 MW; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RETROVIRUSES, pp.757-0, C
Spring Harbor, New York,
[2]
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PIR; T09394; T09394.
HSSP; P03355; 116J.
GO; GO:000416A
                                                                                                    STRAIN=KACC10331 / KXO85;
PubMed=15673718; DOI=10.1093/nar/gki206;
Lee B.-M., Park Y.-J., Park D.-S., Kang H.-W.,
Park I.-C., Yoon U.-H., Hahn J.-H., Koo B.-S.,
Park H.-S., Yoon K.-O., Kim J.-H., Jung C.-H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Appendix 2: Retroviral genetic maps.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=39720;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Walleye dermal sarcoma virus.
Viruses; Retroid viruses; Retroviridae; Epsilonretrovirus
                    "The genome sequence of Xanthomonas oryzae the bacterial blight pathogen of rice."; Nucleic Acids Res. 33:577-586 (2005).
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                                                                                                                                                                                                                                                                                                      Name=pilX; OrderedLocusNames=XOO3199;
Xanthomonas oryzae (pv. oryzae).
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q5GXW8_XANOR
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InterPro; IPR001584;
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                                                                                    Go S.-J
                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC
                                                                                                                                                                                                                                                                                  Xanthomonadaceae;
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10-MAY-2005
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GO:0004523; F:INDanuclease H activity; IEA.
GO:0003723; F:RNA binding; IEA.
GO:00037964; F:RNA-directed DNA polymerase activity; GO:0006310; P:DNA recombination; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
GO:0006578; P:RNA-dependent DNA replication; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                    Xanthomonas.
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Last sequence update)
Last annotation updat
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    Genomic DNA
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                                                                                                             у.-В.,
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J.-S.,
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                                                                                                                                                                                                                                                     EMBL; U09264; AARNOOTS
SMR; Q35392; 1-320.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005746; C:mitochondrion; IEA.
GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:0006739; C:mitochondrion; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; F:electron transport; IEA.
GO; GO:0016491; F:electron transport; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006118; P:electron B.A.
InterPro; IPR005798; Cytb_b6_C.
InterPro; IPR005797; Cytb_b6_N.
R Pfam; PF00032; Cytochrom_B_C; 1.
R Pfam; PF00032; Cytochrom_B_N; 1.
PROSITE; PS51003; CYTB_CTER; 1.
PROSITE; PS51003; CYTB_CTER; 1.
PROSITE; PS51002; CYTB_MTER; 1.
                                                                                          Matches
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Best Local
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Best Local (
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Q35392_9
Q35392;
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SEQUENCE
                                                                                                                                                                                     NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- COPACTOR: Binds 2 heme groups noncovalently (By similarity)
-!- SUBUNIT: The main subunits of complex b-cl are: cytochrome cytochrome of and the Rieske protein (By similarity).
-!- SIMILARITY: Belongs to the cytochrome b family.
EMBL; U09264; AAA65036.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
MEDLINE=94356264; PubMed=8075835; DOI=10.1006/mpev.1994.1019;
Avise J.C., Nelson W.S., Sibley C.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoatzin phylogenetic enigma.";
Mol. Phylogenet. Evol. 3:175-184(1994).

-i- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-cl complex), which is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Avise J.C., Nelson W.S., Sibley C.G.; "Why one-kilobase sequences from mitochondrial DNA fail to solve the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2004 (TrEMBLrel. 26,
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les 6; Conserv
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281
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169 AA;
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320 i
                                                                                        Conservative
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                                                                                                              94.9%;
85.7%;
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                                                                                                                                                                                                                                                       Iron; Metal-binding; Mitochondrion;
mbrane; Transport.
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Last
                                                                                        Score 37; DB Pred. No. 2.2e 1; Mismatches
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Pred. No. 1e+02;
1; Mismatches
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; Cuculiformes; Cuculidae;
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RESULT

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Q9ABX1,
AC Q9ABX1,
AC Q9ABX1,
DT 01-JUN-2
DT 01-JUN-2
DT 01-JUN-2
DT 01-JUN-2
DE Hypothet
GN Ordered
OC Caulobac
OC Bacteria
OC Caulobac
OC NCBI Tax
RN [1]
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RP NICHMAN
RA Lisen J.
RA Potocka
RA DeBoy R.
RA DeBoy R.
RA Ermolaev
RA Fraser (
RT "Complete
RL Proc. Na
DR PIR; BB;
DR TIGR; GC
COmplete
SQ SEQUENCI
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13-SEP-2005 (TrEMBLrel. 31
13-SEP-2005 (TrEMBLrel. 31
13-SEP-2005 (TrEMBLrel. 31
Hypothetical protein.
ORFNames=DgeoDRAFT_1858;
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v
                                                                                                                                                                                    US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K.,
Hammon N., Israni S., Pitluck S., Richardson
"Sequencing of the draft genome assembly of I
DSM 11300.";
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STRAIN-ATCC 19089 / CB15;

MEDLINE-21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;

MEDLINE-21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;

Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.

Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phatke N.D. Ely

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

KOlonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,

Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,

Ermoleva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
EMBL; AB005684; AAK22086.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation updat
Hypothetical protein CC0099.
                                                                                                                       NUCLEOTIDE SEQUENCE.
STRAIN=DSM 11300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q4HB55
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                                                    DSM 11300.
                                                                    Larimer F., Land M.; "Annotation of the draft
                                                                                                   US DOE Joint Genome
                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                                          STRAIN-DSM
                                                                                                                                                                                                                                                                                        NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=319795;
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TIGR; CC0099; -.
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Q9ABX1;
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85.7%;
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Pred. No. 90;
1; Mismatches
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3EBA6CA59F7C5166 CRC64;
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P.;
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Matches 6
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Matches 6
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InterPro; IPR000637; A+T hook.
NUCLEOTIDE SEQUENCE.

STRAIN=ARCC 19089 / CB15;

MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;

MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;

Nierman W.C., Peldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

Potocka I., Nelson W.C., Newton A.S., Gwinn M.L., Haft D.H.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,

Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,

Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
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EMBL; AAHE01000002; E
Hypothetical protein.
SEQUENCE 168 AA; 1
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01-FEB-2005 (TrEMBLrel. 29, Last
01-FEB-2005 (TrEMBLrel. 29, Last
Hypothetical protein TTHA1333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Transcriptional regulator, AraC family.
OrderedLocusNames=CC2573;
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Q9A584;
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Q5SIN6;
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6; Conserv
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Similarity 85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caulobacter
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Pred. No. 1.6e
1; Mismatches
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Pred. No. 2e+0
1; Mismatches
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A Uchiyama T., Abe T., Ikemura T., Watanabe K.;

A Uchiyama T., Abe T., Ikemura T., Watanabe K.;

T "Substrate-induced gene-expression screening of environmental T metagenome libraries for isolation of catabolic genes.";

Nat. Biotechnol. 23.88-93(2005).

C .-!- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.

EMBL; AB190318; BAD81009.1; -; Genomic DNA.

R GO; GO:0003700; F:transcription factor activity; IEA.

R GO; GO:000355; P:regulation of transcription, DNA-dependent; IE,

R GO; GO:0006350; P:transcription; IEA.

R GO; GO:0006350; P:transcription; IEA.

R InterPro; IPR005419; LysR subst.

R InterPro; IPR005419; LysR subst.
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GO; GO:0003700; F:transcription factor activity; IE
GO; GO:0003700; F:transcription factor activity; IE
GO; GO:0006355; P:regulation of transcription, DNA-
InterPro; IPR012287; Homeodomain-rel.
InterPro; IPR00105; HTHARAC.
IPR000322; HTHARAC; 2.
PFANN; PR00032; HTHARAC; 2.
PRINTS; PR00032; HTHARAC; 1.
PROSITE; PR001124; HTH ARAC; 1.
PROSITE; PS01124; HTH ARAC; FAMILY 2; 1.
PROSITE; PS01124; HTH ARAC FAMILY 2; 1.
PROSITE; PROSITE; PS01124; HTH ARAC FAMILY 2; 1.
PROSITE; PS01124; HTH A
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01-FEB-2005 (TrEMBLrel. 29, La
01-FEB-2005 (TrEMBLrel. 29, La
Hydrogen-peroxide-inducible ge
Name=bzo32-4;
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Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
EMBL; AE005925; AAK24543.1; -; Genomic_DNA.
PIR; C87568; C87568.
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Q5NTGO;
                                                                                                                                                                                                                                                                                PROSITE; PS50931; HTH LYSR; 1.

DNA-binding; Transcription; Transcription regulation.

SEQUENCE 313 AA; 34191 MW; DF336088553D3092 CRC64;
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Bacteria; environmental
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Pfam; PF03466; LysR substrate;
PRINTS; PR00039; HTHLYSR.
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_9BACT
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RPLPNRP 277
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Last annotation update
genes activator.
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Pred. No. 2.7e
1; Mismatches
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RESULT 12
Q8PLV6_XANAC
ID Q8PLV6_XANAC PRELIMINARY;

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Q84SM1 ORYSA
ID Q84SM1;
AC Q84SM1;
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DT 01-JUN-2
DT 01-JUN-2
DT 01-JUN-2
DT 01-JUN-2
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OC Spermato
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RL Submitte
DR Gramenc;
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RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,

RA Ciapina L.F., Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,

RA Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,

RA Ciapina L.P., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,

RA El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,

RA Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Martins B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

A Martins B.C., Machado M.A., Menck C.F.M., Miyaki C.Y., Moon D.H.,

A Martins B.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

A Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

AN Prindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Takita M.A., Fakita M.A., Tamura R.E., Texeira B.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

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                                                                  Gramene; Q84S
Hypothetical
SEQUENCE 35
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01-JUN-2003 (TrEMBLrel. 24, Last sequence up
01-JUN-2003 (TrEMBLrel. 24, Last annotation
Hypothetical protein OJ1092_A07.118.
Name=OJ1092_A07.118;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embr
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01-OCT-2002
01-OCT-2002
01-MAR-2004
                                                                                                                                                            clone:OJ1092_A07.";
Submitted (JUL-2001) to the
EMBL; AP003866; BAC55662.1;
                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
Sasaki T., Matsumoto T., Yaman
"Oryza sativa nipponbare(GA3)
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein XAC1683.
OrderedLocusNames=XAC1683;
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Ehrhartoideae; Oryzeae; Oryza.
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TICKPAMs; TIGR02001; gcw.chp; 1.
Complete proteome; Hypothetical prote
SEQUENCE 334 AA; 36710 MW; C7449C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 417:459-463(2002).
EMBL; AE011800; AAM36550.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xanthomonas axonopodis (pv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=92829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              щ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                    Q84SM1;
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                                                              ai protein.
352 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55
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                                                                  38261 MW;
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85.7%;
   92
   .3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza.
                                                                                                                                                                                                                                                                                                Yamamoto
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                                                                                                                                                                                               EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       citri).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ۲,
   Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 2;
Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                       genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liliopsida; Poales; Poaceae;
                                                                                                                                                                   Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | protein.
| C7449C413BBFB116 | CRC64;
                                                                  56890C8BBCE0C5F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic_DNA
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                                                                                                                                                                   DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ą
   2;
                                                                                                                                                                                                                                                                 chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                               databases
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Length 352;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002
01-MAR-2002
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q72GL1 THET2 PRELIMINARY;
Q72GL1;
05-JUL-2004 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T. Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; "Complete genomic sequence of the filamentous nitrogen-fixing "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4_80XYBQ
                             Nat. Biotechnol. 22:547-553(2004).
EMBL; AE017307; AAS82179.1; -; Gen
InterPro; IPR002110; ANK.
InterPro; IPR007016; Wzy_C.
Pfam; PF04932; Wzy_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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NUCLEOTIDE SEQUENCE.

MEDLINE=21595285; PubMed=11759840;

Makamura Y., Wolk C.P.,
                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
PubMed=15064768; DOI=10.1038/nbt956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical membrane spanning protein. OrderedLocusNames=TTC1837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004
05-JUL-2004
                                                                                                                                                                                      thermophilus."
                                                                                                                                                                                                                                                                           Henne A., Brueggemann H., Raasch C., Wiezer A.,
Liesegang H., Johann A., Lienard T., Gohl O., M
Jacobi C., Starkuviene V., Schlenczeck S., Denc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus thermophilus (strain HB27 / ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=all1154;
                                                                                                                                                                                                             The genome sequence
                                                                                                                                                                                                                                          Klenk H.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=262724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=103690;
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Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 All1154 protein.
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THET2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; BA000019; BAB73111.1; -; AG1950; AG1950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 RPLPTRP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RPLPSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||:||
RPLPTRP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPLPSRP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8:205-213 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deinococcus-Thermus;
                                                                                                                                                                                      Kramer W., No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel.
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27,
27,
                                                                                                                                                                                                                                          Raasch C., Wiezer A., Hartsch T.,
Lienard T., Gohl O., Martinez-Arias
J., Schlenczeck S., Dencker S., Huber
Merkl R., Gottschalk G., Fritz H.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB Pred. No. 3.8e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                     Genomic_DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42DED3CB4EB8A922 CRC64;
                                                                                                                                                                                                                thermophile Thermus
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0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAA-163 / DSM 7039).
i; Thermales; Thermac
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Database
                                                                                                                                                                                                                              Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                              Run
                                                                                                                                                                                    Post-processing: Minimum Match
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                                                                                                                                                                                                                                                          Total number of
                                                                                                                                                                                                                                                                                                                               Scoring table:
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Perfect score:
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38
1 SRLPPLP 7
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                                                                                                                                                                                                                                                                                   2443163 seqs, 439378781 residues
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(c) 1993 - 2006
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Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	Ü
38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38
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ABR98912	ABR99522	ABU80604	ABU67576	ABU86363	ABU89522	ABU91829	ABU98123	ABU98908	ABU85748	AB033803	ABR94775	ABR75013	ABO02859	ABO08807	ABU80837	ABU92730	ABU96299	ABR68246	ABU89997	ADU020/0
Abr98912	Abr99522	Abu80604	Abu67576	Abu86363	Abu89522	Abu91829	Abu98123	Abu98908	Abu85748	Abo33803	Abr94775	Abr75013	Abo02859	Abo08807	Abu80837	Abu92730	Abu96299	Abr68246	Abu89997	ADU82876
Human	Human	Human	Human	Human	Human	Novel	Novel	Novel	Human	Novel	Human	Human	Human	Human	Human	Human	Novel	Human	Novel	Human
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ALIGNMENTS

RESULT 1 AAB17236 Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IT.; TNF; artagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin I; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; 04-MAY-2000 31-OCT-2000 AAB17236; AAB17236 standard; peptide; 7 AA. 25-OCT-1999; WO200024782-A2. Synthetic. thrombosis; pharmaceutical. SH3 antagonist peptide sequence SEQ ID NO:292. (first entry) 99WO-US025044

23-OCT-1998; 22-OCT-1999; 98US-0105371P 99US-00428082

(AMGE-) AMGEN INC.

Feige U, Liu C, Cheetham ŗ Boone TC;

WPI; 2000-350702/30.

active composition of matter comprising an Fc domain and pharmacologically e peptides, useful for treating cancer and autoimmune diseases.

Claim 39; Page 298; 608pp; English.

The present invention describes composition of matter (I) comprising a Fc domain, pharmacologically active peptides, and linkers. Where (I) is (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1. P3, and P4 = are each independently sequences of pharmacologically act peptides; L1, L2, L3, and L4 = are each independently linkers; and a, an is:

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RESULT 2
ABB73229
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Best Local :
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 multimers. ()
cytostatic, a
antianaemic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNP-alpha inhibitor; interleukin I antagonist; IL-1 antagonist; TMP; TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antiitumour; immunosuppressive; cytostatic; antiinfeammatory; antiinfeatic; antidiabetic; ophthalmological; antianaemic; anorectic; antiinfeatility; haemostatic; dermatological; neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infeatility; obesity; sleep disorder; neurological degenerative disease; anaemia; thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB73229 standard;
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                                                                                                          Novel vehicle-peptide molecule inflammatory and autoimmune dis diabetic retinopathy, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Src homology3
                                                                                                                                                                                                                                                                 03-MAY-2000; 2000US-00563286
                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; mimetic; Fc domain; fusion;
                                                                             Claim
                                                                                                                                                                                                                                                                                                 02-MAY-2001; 2001WO-US014310
                                                                                                                                                                                                                                                                                                                               08-NOV-2001
                                                                                                                                                                                                                                                                                                                                                              WO200183525-A2
                                                                                                                                                                                                                                                                                                                                                                                                           HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               erythropoietin; TPO;
                                present invention describes a vehicle-peptide molecule (I) or its
timers. (I) can have antiinflammatory, antitumour, immunosuppressi
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                                                                                                                                                                                                     Liu
                                                                           Page
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                 antirheumatic,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SH3) antagonist peptide SEQ ID NO:292.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the present invention
                                                                                                                                                                                                       Cheetham JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide;
                                                                           176pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            netic; Fc domain; fusion; immunoglobulin
tumour necrosis factor alpha inhibitor;
antiinflammatory, antitumour, immunosuppressive, ic, antiarthritic, antidiabetic, ophthalmological antiinfertility, haemostatic, dermatological and
                                                                             English
                                                                                                          ty, sleep
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                                                                                                          s multimers useful for treating
, cancer, rheumatoid arthritis,
disorders and infertility.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                              New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region, useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                            mimetic; CDR mimetibody; ger
cardiovascular; infectious;
immunomodulator; cardiant; ()
                                                                                                                                                                                                                                                                                29-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SH3 antagonist
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ73383
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                                                                                                                                                                                                                                                                                                             24-MAR-2003; 2003WO-US009139
                                                                                                                                                                                                                                                                                                                                          16-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                       WO2003084477-A2
                                                                                                                                                                                                                                                   (CENZ ) CENTOCOR INC.
                                                                                                                                                                                         2003-804237/75
                                                                                                                                                                                                                      GA,
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us; malignant; neurologic disease;
t; antimicrobial; cytostatic; neuro
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2e+06;
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This invention relates to novel mammalian CDR mimetibodies, specific portions or variants thereof. Specifically, it refers to an antibody fragment where a protein has been inserted into, or replaces a portion of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which

which

Disclosure;

SEQ

ID NO

838; 97pp;

English

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ARESULT 4
ADJ53017
ID 53017
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XX ADJ5
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Best Local S
Matches 7
This invention relates to CH1 deleted mimetibodies (and the DNA see which encode them), compositions, methods and uses. The invention ruseful for the development of compounds with an immunosuppressive, cardiovascular, cardiant, hypotensive, protective, nootropic, antibacterial, virucide or fungicide activity. In addition, the dissequences may prove useful for gene therapy. The CH1-deleted mimetise useful for diagnosing or treating a disease condition in a cell.
                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    itself comprises at least one human framework region and at least one ligand binding region (LBR). The present invention describes human mimetibodies, including modified immunoglobulins and cleavage products that can be useful in gene therapy and the generation of transgenic plants and animals. Furthermore, the CDR mimetibody is useful for preparing compositions for modulating, treating or reducing the symptoms of immune, cardiovascular, infectious, malignant and/ or neurologic diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, cardiant, antimicrobial, cytostatic and neuroprotective activities. This peptide sequence is an SH3 antagonist peptide sequence used to make a mimetibody of the invention.
                                                                                                                                                                                                                 New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, or neurodegenerative disease or disorder, anemia, cancer, or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hypertension; heart failure; neurodegenerative; multiple sclerosis; dementia; Alzheimer's disease; anaemia; cancerous condition; infectious disease; bacterial infection;
                                                                                                                                                              Claim 3;
                                                                                                                                                                                                                                                                                                                                       Heavner GA,
Kutoloski KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-2002; 2002US-0392431P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JUN-2003; 2003WO-US020347.
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                                                                                                                                                                                                                                                                                                                                                           Knight DM,
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                                                                                                                                                              838;
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RESULT 5
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Best Local S
Matches
                                                                                                                                                               Heavner GA, A
                                                                   New CH1 deleted mimetibody polypeptide and nucleic acid, useful diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic nutritional disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                      antiallergic; muscular Gen; cytostatic; antiinflammatory; neuroleptic; ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor; TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder; dental disorder; oral disorder; dermatological disorder; ear disorder; nose disorder; throat disorder; endocrine disorder; metabolic disorder; gastrointestinal disorder; gynaecological disorder; hepatic disorder; obstetric disorder; haematologic disorder; immunological disorder; allergic disorder; infectious disorder; musculoskeletal disorder; ophthalmological disorder; pediatric disorder; psychiatric disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue, organ or animal, specifically for modulating, treating, alleviating, preventing the incidence or reducing the symptoms of a immune, cardiovascular (for example arrhythmia, hypertension or heafailure), or neurodegenerative (for example multiple sclerosis, dem or AlZheimer's disease) diseases or disorders, anaemia, cancerous conditions, or infectious diseases or disorders, anaemia, viral or fungal infection). The present sequence is that of a peptide which used during the creation of a mimetibody of the invention.
                                                                                                                                         WPI;
                                                                                                                                                                                                                                        28-JUN-2002;
19-SEP-2002;
                                                                                                                                                                                                                                                                                   30-JUN-2003; 2003WO-US020495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
                                                                                                                                                                                                                                                                                                                08-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mimetibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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2002US-0412144P
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Pred. No.
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This invention relates to CH1 deleted mimetibodies which encode them), compositions, methods and uses.

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RESULT 6
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AAW11115
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protein tyrosine kinase; signal transduction; RNA;
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                              AAW11098-W11124 are peptides that bind to the Src SH3 domain. The SH3 binding peptides are useful in modulating signal transduction pathways at the cellular level (especially protein tryrosine kinase-mediated), modulating oncogenic protein activity, or providing compounds for the development of drugs with the ability to modulate broad classes, as well as specific classes, of proteins involved in signal transduction and also specific classes, of proteins involved in signal transduction and also specific classes.
                                                                                                                                                                                                                                                                                                                                                                    Peptide with binding affinity for Src homology region 3 (SH3) domains proteins - useful for e.g. modulating signal transduction pathways at cellular level, esp. protein tyrosine kinase-mediated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUL-1994;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                 Claim 39; Page 83; 116pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-117151/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH3 domain-binding peptide used in signal transduction modulation.
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95US-00483555.
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Matches 7
                           Query Match
Best Local :
                                                                                                                                                                              AAW16924-W16948 are random recombinant peptides derived from one of three peptide libraries, T9, T12 and R8C. The peptides are all SH3 domain-binding peptides. SH3 binding peptides are useful in modulating signal transduction pathways at the cellular level (especially protein tyrosine kinase-mediated), modulating oncogenic protein activity, or providing compounds for the development of drugs with the ability to modulate broad classes, as well as specific dasses, of proteins involved in signal transduction and also for regulating the processing, trafficking or translation of RNA. Conjugates of the peptides with detectable labels or imaging agents are useful for imaging cells, tissues and organs in which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conjugates of the peptides with detectable labels or imaging agents are useful for imaging cells, tissues and organs in which Src or Src-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide with binding affinity for Src proteins - useful for e.g. modulating cellular level, esp. protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
protein tyrosine kinase; signal transduction; RNA processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW16930 standard; peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-117151/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sparks AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       trafficking;
                                                                                                          Sequence 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYNC-) UNIV NORTH CAROLINA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SRLPPLP 7
                                                                                                                                                              Src-related proteins are
Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA,
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                                                                                                             A
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95US-00483555
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                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .0%;
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Pred. No. 19;
0; Mismatches
                           Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 binding
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                                                                                                                                                                expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homology region 3 (SH3) domains signal transduction pathways at kinase-mediated.
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19;
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                                                      Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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RESULT 8
AAW25493
ID AAW25493
ID AAW25493
XX AAW25493
XX Cart
XX Cart
XX Cart
XX Cart
XX Cart
XX Utyrc
XX Unid
XX U097
XX 16-E
XX 16-E
XX 16-E
XX 16-E
XX CY
PF 14-E
XX (CY)
PA (CY)
P
RESULT 9
ADA07698
                                                                                                                                                                                                                                                                                                                                                                                cc conjugated moterns in vention. SH3 (Src homology region 3) binding cc peptides are selected from: (a) peptides which bind the SH3 domain of cortactin; (b) peptides which bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of Nck; (d) peptides which bind the SH3 domain of Nck; (e) peptides which bind the SH3 domain of Nck; (e) peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of plc gamma; (c) peptides which bind the SH3 domain of Nck; (h) peptides which bind the SH3 comain of Ycs; and (i) peptides can be used in the method to dentify inhibitors of their binding to their respective SH3 domains, comparting the SH3 domain. The peptides can also be used to activate Src or Src-related protein tyrosine kinases, to stimulate the immune response by increasing the production of certain lymphokines, e.g. conjugated molecule to certain cellular compartments containing Src or Src related proteins
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                                                                                                                                                               S
                                                                                                                                                                                                                         Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                     Sequence 31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a random peptide recombinant isolated the method of the present invention. SH3 (Src homology region 3) bindi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 5; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Src homology region 3 binding peptide - used to activate Src tyrosine kinase(s) and to stimulate immune response by increasing production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sparks AB,
Rider JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tyrosine kinase; immune response; PLCgamma; p53bp2; Crk; Yes; Grb2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-424972/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW25493 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CYTO-) CYTOGEN CORP.
(UYNC-) UNIV NORTH CAROLINA.
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                                                                                                              19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             אי אומ כס stimulate immune response
lymphokine(s), e.g. interleukin-1.
                                                                                                                                                                                                                      Similarity 7; Conserv
                                                                                                                                                                  SRLPPLP 7
                                                                                                              SRLPPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kay BK, Thorn JM,
                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                              100.0%; Sc
100.0%; Pr
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                                                                                                                                                                                                                                                   Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
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                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                              DB 2;
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18-AUG-1997;
18-AUG-1997;
18-AUG-1997;
18-AUG-1997;
       Fischer CL,
Lafleur DW,
                                                                           (FISC/)
(ROSE/)
(SOPP/)
(RUBE/)
(RUBE/)
(KYAW/)
(LIYY/)
(ZENG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunosuppressive; dermatological; antiinflammatory; antiallergic; antiarthritic; human; autoimmune disease; autoimmune disorder; lupus; transplant rejection; allergic reaction; arthritis; squamous cell E48 antigen.
                                            (LAFL/)
(MOOR/)
(SHIY/)
(OLSE/)
                                                                                                                                                                                                                                                                          08-JUL-1997
18-AUG-1997
                                                                                                                                                                                                                                                                                         08-JUL-1997;
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08-JUL-1997;
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08-JUL-1997
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12-SEP-1997;
                                                                                                                                                                                            18-AUG-1997;
18-AUG-1997;
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18-AUG-1997;
                                                                                                                                                                                                                           18-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein from gene 78,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA07698 standard; peptide; 61
                                                                                                                                                      L2-SEP-1997
                                                                                                                                                               12-SEP-1997;
                                                                                                                                                                      12-SEP-1997
                              BREW/)
                            OLSEN H S.
EBNER R.
BREWER L A.
                                                                                FISCHER C L.
ROSEN C A.
SOPPET D R.
RUBEN S M.
KYAW H.
LI Y.
                                    ZENG Z.
LAPLEUR
MOORE P
SHI Y.
OLSEN H
EBNER R.
       Rosen
Moore
                                                                                                                                                                                                                                                                                                                                                                                                                   2001US-00984490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                           970S-0051919P

970S-0051920P

970S-0051926P

970S-0051928P

970S-0051931P

970S-0051931P

970S-0051931P

970S-0052733P

970S-0052733P

970S-0052793P

970S-0052795P

970S-0052795P

970S-00558684P

970S-005594P

970S-0055964P

970S-0056360P

970S-0056360P
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₽ ₩.
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      PACA
      Soppet DR, Ruben SM, Ky
Shi Y, Olsen HS, Ebner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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      Kyaw H,
ner R, Bı
             Li Y,
             Zeng
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Brewer LA;

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#XFFX#X555555555555555555555555555555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 7
                                                                                                                                             cardiovascular; respiratory; gene therapy; secreted protein; chromosome identification; hybrid mapping; gene expression control; immune system disorder; immunodeficiency; Chediak-Higashi syndrome; autoimmune disease; systemic lupus erythematosus; rheumatoid arthrit multiple sclerosis; haemolytic anaemia; myasthenia gravis; allergic reaction; asthma; inflammatory condition; inflammatory bowel disease; B cell stimulator; T cell activator; blood-related disorder; eosinophilia; thrombosis; thromboembolism; atherosclerosis; myocardial infarction; angina; anaemia; hyperproliferative disorder; cancer; renal disorder; chronic kidney failure; renal tubular acidosis; kidney stone; cardiovascular disorder; respiratory disorder; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel antibody which specifically binds to a secreted protein useful for diagnosing and treating lupus, arthritis, allergic reactions, arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 61
                                                                                                                                                                                                                                                                                                                                                                                                                     immunomodulator; immunosuppressive; antiinflammatory; dermatological; antiarthritic; antirheumatic; neuroprotective; antianaemic; muscular; antiallergic; antiasthmatic; gastrointestinal; anticoagulant; thrombolytic; antiarteriosclerotic; cardiant; cytostatic; nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human secreted protein fragment seqid 630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADN41508 standard; protein; 61
                                                                   US2004044191-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              secreted proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRLPPLP 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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08-JUL-1997
18-AUG-1997
12-SEP-1997
12-SEP-1997
12-SEP-1997
12-SEP-1997
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08-JUL-1997;
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08-JUL-1997;
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08-JUL-1997;
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08-JUL-1997
                                                                                                                                  Fischer
Lafleur
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2001;
                                                                                       New isolated nucleic acid encoding human proteins, useful for treating, preventing or diagnosing e.g. rheumatoid arthritis, multiple sclerosis, anemia, inflammatory bowel disease, atherosclerosis, cancers, chronic
                                                                                                                                                                    (MOOR/)
(SHIY/)
(OLSE/)
                                                                                                                                                                                          (LAFL
                                                                                                                                                                                               (LIYY)
                                                                                                                                                                                                                                 (FISC/)
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                                                                                                                                                                                                                     (RUBE,
                                                                                                                                                      (BIRS/)
                                                                                                                                                                                                             KYAW/)
                                                                                                                     2004-225733/21
                                                                                                                                                     LAFLEUR D W
MOORE P A.
SHI Y.
OLSEN H.
EBNER R.
BIRSE C E.
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RUBEN S M.
KYAW H.
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Moore
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97US-0058785P.
98WO-US013684.
99US-00227357.
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S-0056360P.
S-0058660P.
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S-0055947P.
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Shi Y,
                                                                                                                                   DR, Ruben
Olsen H,
                                                                                                                                   SM, I
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Birse C
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K
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The invention describes novel human secreted proteins and the nucleot encoding them. The polynucleotides are useful in chromosome identification, for radiation hybrid mapping, in controlling gene expression, in gene therapy or as molecular weight markers. The polynucleotides and polypeptides are useful for diagnosing, treating preventing diseases of the immune system, immunodeficiencies, e.g. Chediak-Higashi syndrome, autoimmune diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, haemolytic anaemia or myasthenia gravis, allergic reactions, e.g. asthma,

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Disclosure; SEQ ID NO 630;

372pp; English.

and the nucleotides

The Charles the Salver of

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RESULT 11
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Matches 7
                                                                                                                                 Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibacterial; antiviral; antifungal; antiparasitic; gene therapy; arthritis; Parkinson's; Alzheimer's; autoimmune disease; cancer; psoriasis; inflammatory bowel disease; infection; bacteria; virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory conditions, e.g. inflammatory bowel disease. They can also be used as a stimulator of B cell responsiveness to pathogens or as an activator of T cells. The polynucleotides and polypeptides are also useful for treating or preventing blood-related disorders, e.g. eosinophilia, thrombosis, thromboembolism, atherosclerosis, myocardial infarction, unstable angina or anaemia. They can also be used for treating, preventing or diagnosing hyperproliferative disorders (cancers), renal disorders (chronic kidney failure, renal tubular acidosis or kidney stones), cardiovascular disorders or respiratory disorders. This is the amino acid sequence of a novel human secreted protein fragment. Note: This sequence is available in electronic format from the US patent office at
                                                                                                                                                                                                    07-MAR-2000;
                                                                                                                                                                                                                             05-MAR-2001; 2001WO-US004941
                                                                                                                                                                                       19-MAY-2000;
                                                                                                                                                                                                                                                                                     WO200216439-A2
                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiarthritic;
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                                                                                                                                                             (HYSE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mmunosuppressive;
                                                 treating, e.g., Parkinease, and inflammatory
                                                                                                                                 YT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                 polynucleotide encoding bone marrow derived polypeptides useful
ting, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's
and inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRLPPLP 7
                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRLPPLP 10
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nilarity 100.
Conservative
                                                                                                                                                                                     2000US-00519705
2000US-00574454
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                                                                                                                                                            INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiparkinsonian; neuroprotective; nootropic;
ive; cytostatic; antipsoriatic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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/label=
                                                                                                                                                                                                                                                                                                                       /note= "OTHER= All Xaa's in this sequence are unknown amino acids or the site of a stop codon within the DNA
                                                                                                                                                                                                                                                                                                                            amino acids or
                                                                                                                                                                                                                                                                                                                                                                                                                                        human
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This invention relates to a novel isolated polynucleotide comprising

Claim disease,

20;

SEQ

ID NO 6806;

504pp; English

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RESULT 12
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Best Local
This represents a human secreted protein. The specification provides secreted protein sequences (AAW63681 to AAW63699) encoded by the nucleic acid sequences shown in AAV43601 to AAV43619. The invention provides a method of identifying a secreted polypeptide which is modified by rough microsomes. The secreted proteins can be used in assays to determine biological activities, such as cytokine, cell proliferation, or cellular differentiation activities, tissue growth or regeneration, activin or inhibin activity, chemotactic or chemokinetic activity, haemostatic or thrombolytic activity, receptor/ligand activity, tumour inhibition, or anti-inflammatory activity. The proteins can also be used as biomarkers, to identify tissues or cell types which express the proteins, or a stage-
                                                                                                                                                                                                        Claim 1; Page 53;
                                                                                                                                                                                                                                                        differentiation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Secreted protein; human; cell proliferation; cytokine activity; tissue growth; cellular differentiation; regeneration; activin; chemotactic; haemostatic; thrombolytic; tumour inhibition; anti-inflammatory activity; biomarker.
                                                                                                                                                                                                                                                                           Secreted
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                                                                                                                                                                                                                                                                                                                                                               Escobedo J,
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                                                                                                                                                                                                                                                                                                                                                                                                (CHIR ) CHIRON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secretory differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                   This is the amino acid sequence of a clone of a human secretory signal protein sequence, used in the method of the invention. All of the proteins sexist in the cell membrane, so are considered to be proteins controlling the proliferation and differentiation of the cells. They may be useful as carcinostatic agents or as antigens for preparing antibodies against the proteins. The cDNAs can be used as probes for gene diagnosis and gene sources for gene therapy, as well as for large-scale expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 84; 84pp; English
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Local Similarity tes 7; Conservat
                                                                                                                                                                              the proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins with secretory signal sequences and
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Conservative (
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2.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the amino acid sequence of a clone of a human secretory signal protein sequence, used in the method of the invention. All of the proteins exist in the cell membrane, so are considered to be proteins controlling the proliferation and differentiation of the cells. They may be useful as carcinostatic agents or as antigens for preparing antibodies against the proteins. The cDNAs can be used as probes for gene diagnosis and gene sources for gene therapy, as well as for large-scale expression
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                                         Human PRO polypeptide sequence #171.
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PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
                                                                                     18-DEC-2001
                                                                                                                                   AAU29194;
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dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
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Homo sapiens.

WO200168848-A2

20-SEP-2001.

28-FEB-2001; 2000WO-US005601 2001WO-US006520.

01-MAR-2000; 02-MAR-2000; 03-MAR-2000; 06-MAR-2000; 2000US-0189320P. 2000US-0189328P. 2000WO-US006884. 2000US-0190828P. 2000US-0187202P. 2000US-0186968P.

14-MAR-2000 15-MAR-2000 21-MAR-2000 21-MAR-2000 21-MAR-2000 21-MAR-2000 28-MAR-2000 29-MAR-2000 29-MAR-2000 30-MAR-2000 04-APR-2000 04-APR-2000 11-APR-2000 11-APR-2000 11-APR-2000 2000US-0191007P. 2000US-0191048P.

11-APR-2000; 11-APR-2000; 11-APR-2000; 11-APR-2000; 18-APR-2000; 25-APR-2000; 25-APR-2000; 25-APR-2000; 25-APR-2000; 25-APR-2000; 25-APR-2000; 25-APR-2000; 25-APR-2000; 27-ANY-2000; 28-JUN-2000; 2000US-0191314P
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2000WO-US01328

(GETH J GENENTECH INC.

Pan ξĐ, P, Chen J Smith V, 'n Watanabe Desnoyers L, Goddard A, Godowski PJ, atanabe CK, Wood WI, Zhang Z; Gurney AL;

N-PSDB; 2001-602746/68 AAS46095.

screen Novel nucleic acids encoding PRO polypeptides, used to diagnose the nce of tumors, such as prostate and breast tumors, in mammals and for modulators of the compounds. breast tumors, in mammals and

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Claim 11; Fig 342; 774pp; English.

Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention. The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the anima and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats the animal

> and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders Sequence 220 AA;

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Matches Query Match Best Local 9 Local Similarity hes 7; Conserv 100.0%; Score Pred. NO. 38; 2.7e+02; DB 4; Length 220;

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S09792
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S53919 S49910 T51873

Query Match 100.0%; Score 38; DB 2; Length 360; Best Local Similarity 100.0%; Pred. No. 22;	RESULT 2 \$09792 S09792 hypothetical protein UL29 - human cytomegalovirus (strain AD169) hypothetical protein UL29 - human cytomegalovirus 5 A;Note: host Homo sapiens (man) C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change (c;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change (c;Accession: \$09792 C;Accession: \$09792 R;Chee, M.S.; Bankler, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Clar: Top. Microbiol. Immunol. 154, 125-169, 1990 A;Title: Analysis of the protein-coding content of the sequence (A;Title: Analysis of the protein-coding content of the sequence A;Reference number: \$09749; MUID:90269039; pMID:2161319 A;Accession: \$09792 A;Status: nucleic acid sequence not shown; translation not shown A;Residues: 1-360 < CHE> A;Cross-references: UNIPROT:P16764; UNIPARC:UPI0000137B88; EMBL:2A;Note: this sequence was submitted to the EMBL Data Library, Dec	Watches 7; Conservative 0; Mismatches 0; Indels Qy 1 SRLPPLP 7 Db 5 SRLPPLP 11	153/2; 214/1 ladenosine transferase (rRNA adenosine lo. 0%; Score 38; DB 2; Length 3 y 100.0%; Bred. No. 19; Trafice C. Might be considered to the constant of	L Data Library, February 1997 squence of C. elegans cosmid T03F1. Z20586 y; translated from GB/EMBL/DDBJ JZS JWIPROT:P91424; UNIPARC:UPI0000175301; s: strain Bristol NZ; clone T03F1	ALIGNMENTS 03F1.7 - Caenorhabditis elegans tis elegans equence_revision 15-Oct-1999 #text_change	30 32 84.2 124 2 G87326 hypotheti 31 32 84.2 198 2 E75599 cconserved 32 32 84.2 203 2 D81934 probable 33 32 84.2 203 2 F81171 cryptic p 34 32 84.2 203 2 F81171 nodulin-2 35 32 84.2 223 2 S07315 nodulin-2 36 32 84.2 246 2 F95397 probable 37 38 42 246 2 F95397 hypotheti 38 32 84.2 284 2 G75447 hypotheti 38 32 84.2 343 2 A43448 thrombin 40 32 84.2 432 2 A43448 thrombin 41 32 84.2 447 2 T20249 hypotheti 42 32 84.2 447 2 T3336 43 32 84.2 452 1 S35534 hypotheti 44 32 84.2 525 2 T23304 hypotheti
	D169) ange 09-Jul-2004 M.; Cerny, R.; Horsnell, T. ence of human cytomegalovir shown EMBL:X17403; NID:g59591; PII y, December 1989	0; Gaps 0;	hyltransfera	EMBL:U88169; PIDN:AAB42235.	31-Dec-2004	hypothetical prote conserved hypothet probable periplasm cryptic protein NM nodulin-23 - soybe nodulin - soybean probable haloacid hypothetical prote 3-alpha-galactosyl thrombin receptor GAP-associated tyr hypothetical prote probable cyclin (i adenovirus EIA enh hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote

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hypothetical protein W02A2.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26080
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A;Accession: T22451
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hypothetical protein F8A5.19 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Pate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 (C.Accession: A96632 R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.
                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT: Q9XUB3; UNIPARC: UPI000007A5B9; EMBL: Z82286; PIDN: CAB05309.1 A;Experimental source: clone W02A2 C;Genetics:
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A; Introns: 30/3;
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A;Experimental source: clone F49E12
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A; Accession: T26080
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Pred. No. 50;
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Pred. No.
     C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo
Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A96632
A;Residues: 1.789 <FAV>
A;Cross-references: UNIPARC:UPI000017B6AE;
C;Genetics:
                                                                                                            A;Description: Sequence of A;Reference number: S44617 A;Accession: S44759
                                                                                                                                           R;Pavello, A.D.

R;Pavello, A.D.

Bubmitted to the EMBL Data Library, May 1993

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A;Residues: 1-262 <KAW>
A;Cross-references: UNIPROT:Q9
A;Experimental source: strain
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Ae A;Reference number: A72450; MUID:99310339; PMID:10382966
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A; Residues: 1-249 <STO>
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                                                                                                                                                                                                                                C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 09-Sep-1997 C;Accession: S44759
                                                                                                                                                                                                                                                                          C14B9.5 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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C;Superfamily:
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C;Accession: A72469
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A; Residues: 1-789 < FAV>
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Pred. No. 53;
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EMBL:L15188; NID:g289640; PID:g289646

TO THE PARTY OF TH

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RESULT 9
S77567
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A; Residues: 1-95 < JIN.
A; Residues: 1-95 < JIN.
A; Crosa-references: UNIPROT:075012; UNIPARC:UPI000005308B; EMBL:Z71781
B; Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; He
Eur. J. Biochem. 245, 449-456, 1997
                                                              A;Gene: SGD:MRP10
A;Cross-references:
A;Map position: 4L
                                                                                                                                                                  A;Cross-references:
C;Genetics:
                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 'D',3-14,'XI',17-18,'X',20,'I'
A;Cross-references: UNIPARC:UPI000017833B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Jin, C.; Myers, A.M.; Tzagoloff, A.
Curr. Genet. 31, 228-234, 1997
A;Title: Cloning and characterization of MRP10 a yeast gene
A;Reference number: S77567; MUID:97218168; PMID:9065385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ribosomal protein S37, mitochondrial - yeast (Saccharomyces K, Shlernate names: protein YDL045w-a; ribosomal protein Yms-C;Species: Saccharomyces cerevisiae C;Date: 16-Apr-1997 #sequence revision 16-Apr-1997 #text_charcession: S77567; S78037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A; Ricession: E70620

A; Sterman E70620

A; Sterman E70620
                                                                                                                                                                                                                                                                                                     A; Accession: S78037
                                                                                                                                                                                                                                                                                                                                 A; Title: Identification and characterization of the genes A; Reference number: S78018; MUID:97296414; PMID:9151978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: S77567; A; Accession: S77567
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C;Superfamily:
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: E70620

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Connor, R.; Chalton S.; Smares, C.; Chalton S.; Chalton S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable pheT protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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Matches 6
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mitochondrion; protein
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85.7%;
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Pred. No. 1.8e
1; Mismatches
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Pred. No. 1.
   biosynthesis;
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R;Robison, K.
submitted to the EMBL Data

Library,

September

21-Jan-2000 #text_change

A; Reference number: A; Accession: T45181

A;Status:

preliminary; e type: DNA

translated

from

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C;Accession: G25035
R;Mankovich, J.A.; Hsu, C.H.; Konisky, J.
J. Bacteriol. 168, 228-236, 1986
A;Title: DNA and amino acid sequence analysis of structural A;Reference number: A91822; MUID:87008385; PMID:3531169
A;Accession: G25035
A;Molecule type: DNA
A;Residues: 1-102 kMAN>
hypothetical protein u1756m [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_chan: C;Accession: T45181
                                                    RESULT
T45181
                                                                                                                                                                                                                                                                                                                                                             hypothetical protein 2 - Bscherichia coli plasmid Colib C;Species: Escherichia coli C;Date: 24-Jan-1988 #sequence_revision 24-Jan-1988 #text_change C;Accession: H25035
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A;Reference number: A91822;
A;Accession: H25035
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C;Genetics:
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A;Residues: 1-102 <M
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R;Mankovich, J.A.; Hsu, C.H.; Konisky,
J. Bacteriol. 168, 228-236, 1986
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                                                                                                                                                                              Local Similarity
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MUID:87008385; PMID:3531169
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Query Match Best Local

Matches

Local Similarity 100.0%; Pred. No. 33 nes 6; Conservative 0; Mismatches

89.5%; Score 34; DB 2; 100.0%; Pred. No. 33;

Length 114; 0; Indels

0,

Gaps

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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A38550; MUID:20512582; PMID:11058132
A;Accession: A83970
                         RESULT 15
E83058
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C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: C83845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q9K9T4; UNIPARC:UPI00000C3F39; GB:AP001515; GB:BA000004; A;Experimental source: strain C-125
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A;Molecule type: DNA
A;Residues: 1-235 <STO>
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83845
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hypothetical protein PA4705 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-293 <STO>
                                                                                                                                                                                                                                                                                                                 ;Superfamily: superoxide dismutase (Mn)
                                                                                                                                                                                                                                                                                                                                                                                        Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                          ;Cross-references: UNIPROT:Q9KCK8; UNIPARC:UPI00000C3C25; GB:AP001512; GB:BA000004; NII
;Experimental source: strain C-125
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A;Residues: 1-114 <KEI>
A;Cross-references: UNIPROT:Q49956; UNIPARC:UPI0000D4395; EMBL:U15180; PIDN:AAA62893.1
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathonic complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathonic complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathonic complete description of Pathonic Complete Sequence of Pseudomonas aeruginosa PA01, an opportunistic pathonic complete description of Pathonic Complete Sequence of Pseudomonas aeruginosa PA01, an opportunistic pathonic complete description of Pathonic Complete Sequence of Pseudomonas aeruginosa PA01, an opportunistic pathonic complete description of Pathonic Complete Sequence of Pseudomonas aeruginosa PA01, an opportunistic pathonic complete description of Pseudomonas aeruginosa PA01, an opportunistic pathonic complete description of Pseudomonas aeruginosa PA01, an opportunistic pathonic complete description of Pseudomonas aeruginosa PA01, an opportunistic pathonic complete description of Pseudomonas aeruginosa PA01, an opportunistic pathonic complete description of Pseudomonas aeruginosa PA01, an opportunistic pathonic complete description of Pseudomonas aeruginosa PA01, an opportunistic pathonic complete description of Pseudomonas aeruginosa PA01, an opportunistic complete description of Pseudomonas aeruginosa PA01, an opportunistic complete description of Pseudomonas aeruginosa PA01, and opportunistic complete description of Pseudomonas aeruginosa aerugino
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: E83058
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
.; Lory, S.; Olson, M.V.
Search completed: April Job time : 3.14529 secs
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A; Residues: 1-295 <STO>
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17 SQLPPLP 23
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Pred. No. 89;
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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  99h8w6
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RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Jamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa M.,
RA Yamazaki M., Ninomiya K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Tmose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Misushima Y., Satoh N., Tashiro A., Tarigami A., Fujiwara T.,
RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Akawabata A., Hikiji T., Robatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Nokitani R., Kawakami T., Natiano T., Morinaga M., Sasaki M.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
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WEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,

Chen J., Chow B., Chui C., Crowley C., Currell B., Dewel B., Dowd P.,

Baton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

Huang A., Kim H.S., Kilmowski L., Jin Y., Johnson S., Lee J.,

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Huang A., Kim H.S., Kilmowski L., Jin Y., Johnson S., Lee J.,

Weeds L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,

Wandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,

Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,

Wood W.I., Godowski P.J., Gray A.M.;

"The secreted protein discovery initiative (SPDI), a large-scale

effort to identify novel human secreted and transmembrane proteins: a
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"A cellular repressor of EIA-stimulated genes
by E2F.";
Mol. Cell. Biol 17
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MEDLINE=98378515; PubMed=9710587;
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                                "Complete
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Genome Res. 13:2265-2270(2003).
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hadeh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rida S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Shevin J.E., Jones S.J.M., Smallus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnertch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA Chimeration and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN 161
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                     EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20273225; PubMed=10815803; DOI=10.1038/sj.onc.1203529; Veal E., Groisman R., Eisenstein M., Gill G.; "The secreted glycoprotein CREG enhances differentiation of NT human embryonal carcinoma cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=15340161; DOI:
Zhang Z., Henzel W.J.
"Signal peptide predi
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SUBCELLULAR LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transcriptional control interaction with IGF2R.
                AF084523; AAC34861.1;
AX359071; AAQ89430.1;
AK095456; BAC04550.1;
AL031733; CAB42866.1;
BC006786; AAH06786.1;
BC008628; AAH08628.1;
                                                                                                                                                                                                                                                                                       Swiss-Prot entry is copyright. It is produced through a deen the Swiss Institute of Bioinformatics and the EMBL
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Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.

EMBL; AC159417; AAX69693.1; -; Genomic_DNA.

DR GO:00003076; F.nuclear mRNA splicing, via spliceosome; IEA.

DR GO:0000398; P:nuclear mRNA splicing, via spliceosome; IEA.

DR InterPro; IPR012677; a b plait nuc bd.

DR InterPro; IPR010504; RNPI_RNA_bd.
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                         25-OCT-2004 (TYEMBLrel. 28, Created)
25-OCT-2004 (TYEMBLrel. 28, Last sequence update)
25-OCT-2004 (TYEMBLrel. 28, Last annotation update)
Hypothetical protein CBG11970 (Fragment).
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60; GO:0003702; F:RNA polymerase II transcript.

GO: GO:0003714; F:transcription corepressor ac

GO: GO:0008283; P:cell proliferation; TAS.

GO: GO:0007275; P:development; TAS.

GO: GO:0006357; P:regulation of transcription

GO: GO:0006377; P:regulation of transcription

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R EMBL; CAACO1000059; CAE66633.1; -; Genomic DNA.

RGO; GO:0008168; F:methyltransferase activity; IEA.

GO; GO:0000179; F:rENA (adenine-NG,NG-)-dimethyltransferase a.

GO; GO:0000179; F:rENA methyltransferase activity; IEA.

GO; GO:00001540; F:rENA methyltransferase activity; IEA.

GO; GO:0000154; P:rENA modification; IEA.

GO; GO:0000154; P:rENA modification; IEA.

RR GO; GO:0000154; P:rENA processing; IEA.

RR GO; GO:0006364; P:rENA processing; IEA.

RR GO; GO:0006364; P:rENA processing; IEA.

RR GO; GO:0006364; P:rENA DIMETH; I.

RR FAGN; SMO0650; rADC; 1.

RR SMART; SMO0650; rADC; 1.

RR PROSITE; PS01131; RRNA_DIMETH; 1.

RPROSITE; PS01131; RRNA_DIMETH; 1.

RPROSITE; PS01131; RRNA_DIMETH; 1.

RPROSITE; PS01131; RRNA_B DIMETH; 1.
Alcendor D.J., M
J. Gen. Virol. 8
-!- SIMILARITY: |
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01-AUG-1990 (Rel
10-MAY-2005 (Rel
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_UL29_!
                                                                                                                               GENOME REANNOTATION.
MEDLINE=22421467; PubMed=12533697; DOI=10.105
MEDLINE=22421467; PubMed=12533697; DOI=10.105
Davison A.J., Dolan A., Akter P., Addison C.,
Alcendor D.J., McGeoch D.J., Hayward G.S.;
"The human cytomegalovirus genome revisited:
chimpanzee cytomegalovirus genome.";
J. Gen. Virol. 84:17-28(2003).
                                                                                                                                                                                                                                                                                                           Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerr Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barre "Analysis of the protein-coding content of the sequence of tytomegalovirus strain AD169 "; Curr. Top. Microbiol. Immunol. 154:125-169(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis briggsae.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE (MEDLINE=90269039; PubMed=2161319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cytomegalovirus (strain AD169)
Viruses; dsDNA viruses, no RNA stage;
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry
                                                                     Davison A.
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(Rel. 47, Last annotation update)
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                    Dolan A., Akter P.,
McGeoch D.J., Hayw
84:1053-1053(2003)
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  herpesviruses
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                                                                                                                                                                                                                                            DOI=10.1099/vir.0
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Hypothetical protein.
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01-OCT-2003 (
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STRAIN=Toledo;

Brondke H., Schmitz B., Shenk T., Doerfler W.;

Submitted (NOV-2003) to the EMBL/GenBank/DDBJ

EMBL; AY223529; AAO/73458.1; -; Genomic_DNA.

EMBL; AY286471; AAS48939.1; -; Genomic_DNA.

InterPro; IPR003360; US22.

Pfam; PP02393; US22; 1.

Pfam; PP02393; US22; 1.
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10-MAY-2005
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Komazin G., Ptak R.G., Emmer B.T., Townsend

"Resistance of human cytomegalovirus to the

ribonucleoside maribavir maps to UL27.";

J. Virol. 77:11499-11506(2003).
                                                                                                                                                                                                                                                                                                                                                                                                             Name=UL29; ORFNames=HHV5gp035;
Human cytomegalovirus (HHV-5) (Human herpesvirus 5).
Viruses; dsNA viruses, no RNA stage; Herpesviridae;
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MCBI_TaxID=10359;
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Q6XNK8;
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S09792; S09792.
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RX PubMed-14702039; DOI=10.1038/ng1285; PubMed-14702039; DOI=10.1038/ng1285; RX PubMed-14702039; DOI=10.1038/ng1285.
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Ra Wakamatsu A., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Ra Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Ra Ra Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Ra Niratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Ra Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta M., Sato K., Tanikawa M., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Ra Qmaraxi M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa Y., Ra Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Ra Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Ra Kusano J., Kanehori K., Takahashi Pujii A., Hara H., Tanase T.-O., Ra Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Sano S., Togiya S., Komai F., Hara R., Sasaki N., Aotsuka S., Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Ra Moriya S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H., Ra Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H., Ra Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H., Ra Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yanazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Ra Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
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Q9H8W6;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ13171.
Hypothetical protein FLJ13171.
Homo sapiens (Human).
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PROSITE; PS01131; RRNA A DIMETH; 1.

Complete proteome; Hypothetical pro
SEQUENCE 367 AA; 41893 MW; FD24
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WormBase; WBGene00020189; T03F1.7.
WormPep; T03F1.7; CE30685.
GO; GO:0000179; F:rRNA (adenine-N6,N6-)-dimethyltransferase
GO; GO:0000849; F:rRNA methyltransferase activity; IEA.
GO; GO:0000154; P:rRNA modification; IEA.
InterPro; IPR01737; RRNA meth_trans.
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Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
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Science 282:2012-2018(1998).
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PIR; T29195; T29195.
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Pred. No. 1.9e+02;
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014498;
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
110-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                             The German cDNA Consortium;
Ansorge W., Krieger S., Regiert T., Rittmueller C., Schwager B.,
Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR858921; CAH91119.1; -; mRNA.
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EMBL; AK023233; BAB14483.1; -; mRNA.
InterPro; IPR004018; RPEL_repeat.
Pfam; PF02755; RPEL; 2.
SMART; SM00707; RPEL; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence up
01-FEB-2005 (TrEMBLrel. 29, Last annotation
Hypothetical protein DKFZp469H1423.
Name=DKFZp469H1423;
                         Homo sapiens
Eukaryota; Me
                                                  ISLR precursor.
Name=ISLR; ORFNames=UNQ189;
                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q5RAU1;
01-FEB-2005
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                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
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                         Metazoa;
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             Euarchontoglires;
                         Chordata;
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Pred. No.
             Craniata; Vertebrata; Euteleostomi;
oglires; Primates; Catarrhini; Homin
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Lu. No. 2e+02;
Mismatches
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                                                                             sequence update)
annotation updat
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             Hominidae;
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AC QS
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R HGNC; HGNC:6133; ISLR.

GG; GO:0005515; F:protein binding; TAS.

R GG; GO:0007155; P:cell adhesion; TAS.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR003591; LRR.

R InterPro; IPR003591; LRR.

R Pfam; pP00560; LRR 1; 5.

R PRINTS; PR00019; LEURICHRPT.

R PROSITE; PS50835; IG LIKE; 1.

I B Potential.

O SEQUENCE 428 AA; 45997 MW; 3163F89D59F6F3A4 CRC64;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P. Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S., Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H., Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H., Watanabe C., Wieand D., Woods K., Xie M.-H., Wood W.I., Godowski P.J., Gray A.M.; The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins:
  Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B. Osanger A., Fobo G., Han M., Wiemann S.; Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 13:2265-2270(2003).
EMBL; AB003184; BAA22848.1; -;
EMBL; AY358871; AAQ89230.1; -;
HSSP; P07359; 1M0Z.
                                                                                  The German
                                                                                                                  TISSUE=Cortex;
                                                                                                                                                                                           NCBI_TaxID=9600;
                                                                                                                                                                                                                            Pongo
                                                                                                                                                                                                                                                                                                                                              Name=DKFZp459M1420;
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                                                                                                                                                                                                                                                            Eutheria;
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                                                       Weil B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 428
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                                                          Amid
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InterPro; IPR003598; Ig c2.
InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR. Cterm.
InterPro; IPR003591; LRR. typ.
Pfam: PF00560; LRR.1; 5.
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619 CAEEL
020619 CAEEL PRELIMINARY;
020619;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-MAR-2004 (TrEMBLrel. 2
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SEQUENCE
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PRINTS, PR00019; LEURICHRPT.
SMART; SM00018; LRR TYP; 5.
SMART; SM000369; LRR TYP; 5.
SMART; SM00020; LRRCT; 1.
PROSITE; PS50835; IG_LIKE; 1.
Hypothetical protein; Immunoglobulin domain; Leucine-rich repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Testis cDNA clone: QtsA-10310, similar to human hypothetica:
FLJ13171 (FLJ13171),
Macaca fascicularis (Crab eating macaque) (Cynomolgus monke)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleon
Mammalla; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K. "Substitution rate and structural divergence of 5'UTR evolu Comparative analysis between human and cynomolgus monkey of Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   International consortium for macaque cDNA "DNA sequences of macaque genes expressed evolutionary implications.";
Submitted (JUN-2005) to the EMBL/GenBank/I
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Pred. No.
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Pred. No. 2.8e+02;
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ertebrata; Euteleostomi;
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in brain or
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L Science 282:2012-2018 (1998).

C -- SUBCELLULAR LOCATION: Nuclear (By similarity).

C -- SUBCELLULAR LOCATION: Nuclear (By similarity).

R PIR; T72451; T72451.

R PIR; T72452; T72451.

R HSSP; Q16254; 1CF7.

R HSSP; Q16254; 1CF7.

R HSSP; Q16254; CF7.

R MormBase; WBGene0009899; F49E12.6.

R WormBase; WBGene0009899; F49E12.6.

R WormBase; WBGene0009899; F49E12.6.

R GO; GO:0000563; C:transcription factor complex; IEA.

R GO; GO:0000567; C:transcription factor activity; IEA.

R GO; GO:0000567; C:transcription factor activity; IEA.

R GO; GO:0000555; p:regulation of transcription, DNA-depen

R GO; GO:0006355; p:regulation of transcription, DNA-depen

R GO; GO:0006355; p:regulation of transcription, DNA-depen

R GO; GO:000310; E2F TDP.

R InterPro; IPR003316; E2F TDP.

R Complete proteome; DNA-binding; Hypothetical protein; Nu

Transcription; Transcription
                                          MEDLINEs-2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Stlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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Caenorhabditis elegans.
Eukaryota, Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
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MEDLINE=99069613; PubMed=9851916;
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Mammalia; Eutheria;
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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Q6NUN6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Bouffard
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Q68DD4 HUMAN
ID Q68DD4 H
AC Q68DD4;
DT 25-OCT-2
DT Mypothet
GN Name=DKF
OS Homo sap
OC Eukaryot
OC Mammalia
OC Homo.
OX NCBI_Tax
RN [1]
RC TISUE=F
RG The Germ
RA Bloecker
RA Submitte
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DR InterPro
DR Pfam; PF
DR SMART; SC
SQ SEQUENCE
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC066508; AAH68508.1; -; mRNA.
InterPro; IPR004018; RPEL_repeat.
Pfam; PF02755; RPEL; 1.
SMART; SM00707; RPEL; 2.
PROSITE; PS1073; RPEL; 2.
SEQUENCE 630 AA; 69243 MW; 5FA0C75B4535C010 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGBDD4 HUMAN PRELIMINARY; PRT; 654 AA. Q6BDD4; QCBDD4; 25-OCT-2004 (TrEMBLrel. 28, Created) 25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Hypothetical protein DKFZp686L07205.
                                                                                                                                                                                                                       Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases. EMBL; CR749449; CAH18286.1; -; mRNA. InterPro; IPR004018; RPEL_repeat. Pfam; PF02755; RPEL; 2. SMART; SM00707; RPEL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 654 AA; 72716 MW;
                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
TISSUE=Fetal brain;
The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Local Similarity 100.0%;
les 7; Conservative
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3.7e+02;
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Pseudomon Lung canc

The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently linkers; and a, b, peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,

Claim 39; Page 299; 608pp; English.

active Novel

composition of matter comprising an Fc peptides, useful for treating cancer a

c domain and pharmacologically and autoimmune diseases.

4 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25 .
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Abp97714	Aab19934	Aag25783	Aag45922	Aag25784	Aag45923	Aau98427	Abm86753	Adt56743	Aag14087	Aag50444	Aag50445	Aag14088	Abg18051	Abg09606	Adm05717	Adi54470	Aau87155	Abm94494	Aag14089	Aag50446
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RESULT 1 AAB17237 ID AAB1 XX AAB1 XX AAB1 XX AAB1 XX AAB1 XX Modi XW Modi XW Modi XW Inhi XW I Modified peptide; therapeutic agent; fusion; Pc domain; cancer; autoimmune disease; cycostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLAn; mimmetic; IL-1; TNF; antagonist; Minhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; 04-MAY-2000 WO200024782-A2 Synthetic. thrombosis; pharmaceutical. SH3 antagonist peptide sequence 31-OCT-2000 AAB17237; AAB17237 standard; peptide; 7 AA (first entry) SEQ ID NO:293.

MMP;

23-OCT-1998; 22-OCT-1999;

98US-0105371P 99US-00428082 99WO-US025044

25-OCT-1999;

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(AMGE-) AMGEN INC.

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       erythropoletin; TPO; tumour necrosis factor alpha inhibitor; TMF; TMF-alpha inhibitor; interleukin i antagonist; IL-1 antagonist; TMP; TPO mimetic peptide; BPO mimetic peptide; BMP; VBGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antirheumatic; antiinfertility; antidiabetic; ophthalmological; antianaemic; anorectic; antiinfertility; demonstatic; dermatological; neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the present invention
                                                                                                                      Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
multimers. (I) can have antiinflammatory, antitumour, immunosuppressive, cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
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pietin; TPO; tumour necrosis factor alpha inhibitor;
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ilarity 100.0%;
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                                                                                                                                                                                                                         Cheetham
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                                                                                 176pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metastatic tumour; systemic lupus
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                                                    describes a vehicle-peptide molecule (I)
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This invention relates to novel mammalian CDR mimetibodies, specific portions or variants thereof. Specifically, it refers to an antibody fragment where a protein has been inserted into, or replaces a portion of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which

Disclosure;

SEQ

ID NO

839; 97pp;

English.

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cc prophylactic agent as well as for screening purposes. (I) is useful for cc diagnosing diseases characterised by dysfunction of their associated protein of interest, for identifying normal or abnormal proteins of interest in a biological sample. Additionally, (I) is useful cc proteins of interest in a biological sample. Additionally, (I) is useful cc for treating inflammatory and autoimmune diseases, tumour growth, cancer, cc remunatoid arthritis, diabetic retinopathy, obseity, sleep disorders, cc infertility, and neurological degenerative diseases. (I), comprising EPO-cc mimetic compounds are useful for treating disorders characterised by low cred blood cell levels such as anaemia. The TPO-mimetic comprising cc compounds are useful for treating conditions that involve an existing megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet cumour which result in thrombocytopaenia, spastic anaemia, metastatic cumour which result in thrombocytopaenia, spastic anaemia, metastatic cumour which result in thrombocytopaenia, spastic anaemia, metastatic cumour which result in thrombocytopaenia, spastemic lupus erythematosus, cr represent amino acid and nucleic acid sequences used in the exemplification of the present invention
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New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding regionseful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mimetic; CDR mimetibody; gene therapy; transgenic; immune; cardiovascular; infectious; malignant; neurologic disease; immunomodulator; cardiant; antimicrobial; cytostatic; neuro
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cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, antibacterial, virucide or fungicide activity. In addition, the discloss sequences may prove useful for gene therapy. The CHI-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell,
                                                                                                          This invention relates to CH1 deleted mimetibodies (and the DNA se which encode them), compositions, methods and uses. The invention useful for the development of compounds with an immunosuppressive,
                                                                                                                                                                                                                                                                                                          New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, or neurodegenerative disease or disorder, anemia, cancer, or infectious
                                                                                                                                                                                                                                Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypotensive; neuroprotective; nootropic; antibacterial; fungicide; gene therapy; immune disorder; cardiovasculaarrhythmia; hypertension; heart failure; neurodegenerat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kutoloski KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUN-2002; 2002US-0392431P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ53018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CENZ )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CENTOCOR INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Knight
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                                                                                                                                                                                                                                NO 839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                       129pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ghrayeb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
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Pred. No.
                                                                                                                                                                                                                          English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide SeqID839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorder; cardiovascular disease; failure; neurodegenerative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scallon
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                                                                                                                                       on may be
                                                     disclosed
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RESULT 5
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Best Local 9
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                                                                                                                                                                        Heavner GA, K
                                                                                                                                                                                                                                                                                                                                                                                                                                         ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor; TWF; cytokine; bone disorder; joint disorder; cardiovascular disorder; dental disorder; oral disorder; dermatological disorder; ear disorder; nose disorder; throat disorder; endocrine disorder; metabolic disorder; gastrointestinal disorder; gynaecological disorder; hepatic disorder; obstetric disorder; haematologic disorder; mimunological disorder; allergic disorder; infectious disorder; musculoskeletal disorder; oncological disorder; neurological disorder; nutritional disorder; ophthalmologic disorder; pediatric disorder; psychiatric disorder;
                                                                                 New CH1 deleted mimetibody polypeptide and nucleic acid, useful idiagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gymecologic, infectious, neurologic
                                                                              diagnosing, preventing or treendocrine, gastrointestinal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; gynaecological-Gen; hepatotropic; haemostatic; immunomodulator; antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;
                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                   28-JUN-2002;
19-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue, organ or animal, specifically for modulating, treating, alleviating, preventing the incidence or reducing the symptoms of a immune, cardiovascular (for example arrhythmia, hypertension or hea failure), or neurodegenerative (for example multiple sclerosis, dem or Alzheimer's disease) diseases or disorders, anaemia, cancerous conditions, or infectious diseases (for example bacterial, viral or fungal infection). The present sequence is that of a peptide which
                                                                                                                                                                                                                                                                                               30-JUN-2003; 2003WO-US020495
                                                                                                                                                                                                                                                                                                                              08-JAN-2004
                                                                                                                                                                                                                                                                                                                                                           WO2004002424-A2
                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CH1 deleted mimetibody; osteopathic; cardiovascular-Gen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CH1 deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ51979;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7 AA;
                                                                                                                                                                                                                       (CENZ ) CENTOCOR INC.
                                                                                                                                                 2004-082872/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   during the creation of a mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                   disorder; pulmonary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mimetibody-related peptide SeqID839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                   2002US-0392431P
2002US-0412144P
                                                                                                                                                                                         Knight
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                                                                                                                                                                                         Ghrayeb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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the DNA sequences invention may be

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CC gastrointestinal-Gen, gynascological, anuticuty, enductive controlled that controlled the controlled to the controlle
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Best Local :
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                     AAW11098-W11124 are peptides that bind to the Src SH3 domain. The SH3 binding peptides are useful in modulating signal transduction pathways the cellular level (especially protein tyrosine kinase-mediated), modulating oncogenic protein activity, or providing compounds for the development of drugs with the ability to modulate broad classes, as well as specific classes, of proteins involved in signal transduction and all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7
                                                                                                                                                                                                                                                                                                                               Peptide with binding affinity for Src homology region 3 proteins - useful for e.g. modulating signal transductic cellular level, esp. protein tyrosine kinase-mediated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Src
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-117151/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUL-1994;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Src; 8H3; Src homology region 3; binding affinity; oncogenic protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW11120
                                                                                                                                                                                                                                                                   Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein tyrosine kinase; signal transduction; RNA processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYNC-) UNIV NORTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SH3
                                                                                                                                                                                                                                                                40; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    μ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RALPSPP 7
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95US-00483555.
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                                                                                                                                                                                                                                                                116pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide
                                                                                                                                                                                                                                                                English.
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Pred. No.
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trafficking or
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                                                                                                                                                                                                                                                                                                                                      signal transduction kinase-mediated.
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                                                                                                                                                                                                                                                                                                                                                                                                         (SH3) domains
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Score 38; DB Pred. No. 28; Mismatches

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RESULT 7
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Best I
                                AAW16924-W16948 are random recombinant peptides derived from one of three peptide libraries, T9, T12 and R8C. The peptides are all SH3 domain-binding peptides. SH3 binding peptides are useful in modulating signal transduction pathways at the cellular level (especially protein tyrosine kinase-mediated), modulating oncogenic protein activity, or providing compounds for the development of drugs with the ability to modulate broad classes, as well as specific classes, of proteins involved in signal transduction and also for regulating the processing, trafficking or translation of RNA. Conjugates of the peptides with detectable labels or imaging agents are useful for imaging cells, tissues and organs in which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conjugates of the peptides with detectable labels or imaging useful for imaging cells, tissues and organs in which Src or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins
                                                                                                                                                                     Disclosure; Fig 1; 116pp; English.
                                                                                                                                                                                            Peptide with binding affinity for Src proteins - useful for e.g. modulating cellular level, esp. protein tyrosine
                                                                                                                                                                                                                                                                                                                       22-JUL-1994;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                    08-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trafficking;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
protein tyrosine kinase; signal transduction; RNA processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Random recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW16931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW16931 standard; peptide; 26
                                                                                                                                                                                                                                                WPI; 1996-117151/12
                                                                                                                                                                                                                                                                       Sparks AB
                                                                                                                                                                                                                                                                                                                                                             24-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                            WO9603649-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     are expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                       Kay BK,
                                                                                                                                                                                                                                                                                                NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
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95US-00483555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "X is undefined in the specification"
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                        proteins
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Pred. No.
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                         expressed
                                                                                                                                                                                              homology region 3 (s
signal transduction
kinase-mediated.
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                                                                                                                                                                                                           (SH3) domains
on pathways at
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Src-related
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RESULT 8
AAW25494
ID AAW2
                                                                The present sequence represents a random peptide recombinant isolated by CC the method of the present invention. SH3 (Src homology region 3) binding CC peptides are selected from: (a) peptides which bind the SH3 domain of CC Cortactin; (b) peptides which bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of Nck; (c) CC SH3 domain of Src; (e) peptides which bind the SH3 domain of PLC gamma; CC (f) peptides which bind the SH3 domain of PLC gamma; CC (f) peptides which bind the SH3 domain of CC (f) peptides which bind the SH3 domain of Yes; and (i) peptides which bind the amino-terminal SH3 domain of Grb2. The purified binding peptides can be used in the method to (c) dontify inhibitors of their binding to their respective SH3 domains, CC which could be used to modulate the pharmacological activity of proteins CC or polypeptide containing the SH3 domain. The peptides can also be used to activate Src or Src-related protein tyrosine kinases, to stimulate the containing the SH3 domain of certain lymphokines, e.g. CC conjugated molecule to certain cellular compartments containing Src or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              문
Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       Src homology region 3 binding peptide - used to kinase(s) and to stimulate immune response by ir certain lymphokine(s), e.g. interleukin-1.
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 5; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-424972/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cortactin; SH3 domain;
tyrosine kinase; immuno
PLCgamma; p53bp2; Crk;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Random peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW25494 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sparks AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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UNIV NORTH CAROLINA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SH3 domain; binding peptide; Src homology region 3; inase; immune response; lymphokine; interleukin 1; Nck; Abl; p53bp2; Crk; Yes; Grb2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kay BK,
100.0%; (ilarity 100.0%; (Conservative 0;
                                                               Ä
                                                                                            proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinant clone T9.SRC3.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Score 38; DB Pred. No. 28; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quilliam LA,
                              DB
                              2;
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                              Length 26
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RESULT 9
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                                                                                                                           AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted protein genes, and AAG73346-AAG73448 represent the proteins they encode. AAG73449-AAG73519 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, corresponding or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions conditions, e.g., by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, eathma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cartification disorders, angiogenic disorders, kidney disorders.
                          gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due sunburn, to maintain organs before transplantation, for supporting ceculture of primary tissues, to regenerate tissues, to identify their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; ALDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; tumour; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 543-544; 604pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preventing, diagnosing an and diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAH32586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-1999; 99US-0164735P
27-JUL-2000; 2000US-0221193P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-NOV-2000; 2000WO-US030653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human gene 14-encoded secreted protein HBXFZ38, SEQ ID NO:181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG73409 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
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RESULT 10
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ID ABG64
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as a food additive or preservative to modify storage properties.
Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                   The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosting disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocraine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Albumin fusion protein; therapeutic protein; human albumin; thousan serum albumin; HSA; cancer; reproductive disorder; disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG64232 standard; protein; 78 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; antiinfertility; antiinflammatory; antiulcer;
immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human albumin
                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                          albumin
                                                                                                                                                                                                                                                                                                                                                New fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-APR-2000;
21-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN
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a food additive or
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7; Conserv
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                                                                                                                                                                                                                                                                             Page 1092; 2102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                           Haseltine
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2000US-0199384P.
2000US-0256931P.
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Creutzfeldt-Jacob
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiparkinsonian; antimicrobial;
                                                                                                                                                                                                                                                                                                                          a therapeutic
                                                                                                                                                                                                                                                                                                                                             for treating disease
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Pred. No.
                                                                                                                                                                                                                                                                                                                          protein.
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79;
  encephalomyelitis,
                                                                                                                                                                                                                                                                                                                                                  e.g.
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                                                                                                                                                                                                                                                                                                                                                     diabetes comprises
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contribution protein comprising the albumin fusion protein can a pharmaceutical carrier; a kit comprising the composition of the albumin fusion protein formula; a method of treating a disease or disorder in a patient comprising the step of administering the albumin comprising a patient with a disease or disorder that is modulated by Therapeutic protein; x, or its fragment or variant; a mucleic acid molecule comprising a polynucleotide fragment or variant; a nucleic acid molecule comprising a polynucleotide comprising the albumin fusion protein; and a host cell comprising the nucleic acid molecule of the albumin fusion protein, and a host cell comprising the nucleic acid molecule of the albumin fusion protein. The albumin fusion protein, and a host cell comprising the protein and its compositions have the following cativities: cytostatic, antianemic, antiarthritic, antiarabetic, antiara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-APR-2000;
25-APR-2000;
21-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
                                                                                                                                                                                                                                                                                                                                                                                                              New albumin fusion proteins, useful for diagnosing, treating, prevent or ameliorating diseases or disorders e.g. cancer, anemia, arthritis, asthma, inflammatory bowel disease or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranquilizer; antidiabetic; anabolic; hypertensive; vulnerary; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          albumin fusion protein; cytostatic; antianaemic; antiarthritic; antiathritic; antiathritic; antiathritic; antibacterial; osteopathic; dermatological; antigout immunosmodulator; antiarrhythmic; cardiant; nootropic; antilipaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Albumin fusion
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                                                                                                                                                                                                                                                                                                                              invention relates to a novel albumin fusion protein.
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO
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2000US-0199384P.
2000US-0256931P.
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Pred.
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No.
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cardiant, nootropic, antilipaemic, nephrotropic, uropathic, anabolic, neuroprotective, antiparkinsonian, tranquilizer, antidiabetic, anabolic,

· Martin Carlo · Martin Carlo

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RESULT 12
ABP71204
ID ABP71
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Best Local S
Matches 7
WPI; 2003-111893/10.
N-PSDB; ABZ58812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S. cinnamoneus cinnamycin cinR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-APR-2003
                                                                    Bibb MJ;
                                                                                                                                                                                                                       29-APR-2002; 2002WO-GB001983
                                                                                                                                                                                                                                                                      07-NOV-2002
                                                                                                                                                                                                                                                                                                                                                              Streptomyces cinnamoneus
                                                                                                                                                                                                                                                                                                                                                                                                         Cinnamycin; bacterium; cinA; cinM; cinX; cinT; cinH; cinY; antibiotic; food additive; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP71204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP71204 standard;
                                                                                                                                                                            27-APR-2001; 2001GB-00010432
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                                                                                                            PLANT BIOSCIENCE LTD WIDDICK D A.
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Propionibacterium acnes vaccinating against and

polypeptides and nucleic acids useful for diagnosing infections, especially useful

for

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RESULT 13
AAU49716
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Best Local :
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                                                                                                          Skeiky YAW, Persing DH L'maisonneuve J, Zhang
                                                                                                                                                                                          21-APR-2000; 2000US-0199047P
02-JUN-2000; 2000US-0208841P
07-JUL-2000; 2000US-0216747P
                                                                                                                                                                                                                                                                                                                                                                                                            SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; BLISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                              N-PSDB;
                                                                              WPI; 2001-616774/71
                                                                                                                                                                                                                                                                                                01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                               Propionibacterium acnes.
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                                                                                                                                                                                                                                                                                                                                                                                                dermatological; osteopathic; neuroprotectant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU49716 standard; protein; 51 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New expression cassettes or genes isolated from Streptomyces cinnamoneus, useful for producing a library of lantibiotic-producing host cells or lantibiotics, which are useful as food additives and antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from S. cinnamoneus 40005 as present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; Fig 20; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 RALPSPP 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 7; Conserv
                                                             AAS59545
                                                                                                                                                             CORIXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                             CORP
                                                                                                                            DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                          Mitcham JL, Wang S
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on the plasmid pDWFT9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB
                                                                                                                            ss,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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RESULT 14
ABM46235
XX PRINTER 
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CP pustulosis hypertosis and osteomyelicis of bone, joints and the central concrous system, however it is particularly involved in the central concrous system, however it is particularly involved in the inflammatory concrous associated with accessing a patient comprises contacting the concept of the invention concrete with a binding agent that binds to the proteins of the invention cand determining the amount of bound protein in the sample. The concrete c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                               Mitcham JL, S.C. Zhang Y, Wang S, Jen C, B, Vallieve-Douglass J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides. The proteins and their associated DNA sequences are use the treatment, prevention and diagnosis of medical conditions caused p. acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABM46235 standard; protein; 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                        New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                              WPI; 2003-381789/36.
N-PSDB; ACF64474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Propionibacterium acnes predicted ORF-encoded polypeptide #10911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-OCT-2001; 2001US-00978825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2002; 2002WO-US032727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003033515-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-)
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                                                                                                                    ptide, useful for diagnosing, pr
stimulating an immune response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RALPAPP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU39105-AAU68017 represent Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ã,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲.
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Pred. No. 1.6e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine.
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1.6e+02;
0;
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Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Benson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carter D;
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Example 1; SEQ

IJ

NO 10911; 1481pp; English

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CC encoding a Propionibacterium acres protein. The invention also relates to golypeptides encoded by the polymucleotides (ARM35624-ABM6435) and to compose the invention also relates to compose the invention of polypeptides. The invention additionally encompasses expression vectors and host cells comprising a golypeptide of the invention comprising a polypeptide of the invention; antibodies against polypeptides of the invention; antibodies against polypeptides of the invention; a comprising a polypeptide of the invention; a comprising a polypeptide of the invention; a composition (comprising T cells prepared comprising T cells prepared the comprising T cells prepared to T cells prepared
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  RESULT 15
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Best Local
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                                     04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiucer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human nervous system related polypeptide SEQ ID NO 4135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB15478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB15478 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 51
                                                                                                                                                                                                                                  16-AUG-2001.
                                                                                                                                                                                                                                                                            WO200159063-A2
                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                         17-JAN-2001; 2001WO-US001334.
                                                                                                                                                                                                                                                                                                                                                             neurological
                                                                                                                                                                                                                                                                                                                   sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3
; 2000US-0179065P.
2000US-0184664P.
2000US-0184664P.
2000US-0186350P.
2000US-0189874P.
2000US-0198123P.
2000US-0205515P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                 disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                 infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75
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Pred. No. 1.6e+02;
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                               nephrotropic; gene therapy; vaccine
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人名英格里斯特古

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us-10-632-388-293.rag
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Nucleic acids e useful for prev and metastases.
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20-OCT 2000;

20-OCT 2000;

20-OCT 2000;

20-OCT 2000;

01-NOV 2000;

08-NOV 2000;

17-NOV 2000;

17
The invention relates to novel genes (ABA11004-ABA21 (ABB14678-ABB18001) useful for preventing, treating medical conditions e.g. by protein or gene therapy. isolated from a range of human tissues disclosed in
                                                                                 Claim
                                                                                                                                                                               WPI; 2001-541565/60.
N-PSDB; ABA11804.
                                                                                                                                                                                                                               Rogen
                                                                                11;
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                                                                                                                              ; acids encoding for preventing,
                                                                                                                                                                                                                                                                HUMAN
                                                                              SEQ
                                                                                                                                                                                                                               Barash
                                                                                                                                                                                                                                                                                           2000US-0241786P

2000US-0241787P

2000US-0241809P

2000US-0241809P

2000US-024221P

2000US-0244617P

2000US-02464776P

2000US-02464778P

2000US-0246523P

2000US-0246523P

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2000US-0246611P

2000US-0249211P

2000US-02591169P

2000US-0251169P

2000US-02511869P

2000US-0251989P

2000US-0251999P

2000US-0251999P

2000US-0251999P

2000US-0251999P

2000US-0251999P

2000US-0251999P
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                                                                                4135;
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                                                                                                                              3224 human
diagnosing
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                                                                              1701pp
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N
                                                                                +
                                                                                                                              nervous system and/or treating
                                                                            Sequence
(ABA11004-ABA21534) and proteins uring, treating or ameliorating reset therapy. The genes are as disclosed in the specification.
                                                                              Listing;
                                                                                                                                antigen polypeptides,
g nervous system cancers
                                                                                English
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207-JUN-2000
28-JUN-2000
30-JUN-2000
30-JUN-2000
07-JUL-2000
11-JUL-2000
11-JU

7000US-0209467P.
7000US-0214886P.
7000US-02114890P.
7000US-02127496P.
7000US-0217496P.
7000US-0217496P.
7000US-0217496P.
7000US-022964P.
7000US-0225213P.
7000US-0225267P.
7000US-02252759P.
7000US-0225757P.
7000US-0225757P.
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7000US-023144P.
7000US-0231443P.
7000US-0231444P.
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7000US-0234499.
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7000US-0

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Search completed: April 4, 2006, 13:07:42 Job time : 5.47251 secs
                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 75 AA;
                                                                                                                                                                                                                                                                    y Match 92.1%;
Local Similarity 85.7%;
hes 6; Conservative
                                                                                                                                  35 RAVPSPP 41
                                                                                                                                                                                                       1 RALPSPP 7
                                                                                                                                                                                                                                                                            Score 35; DB 4; Length 75; Pred. No. 2.3e+02; 1; Mismatches 0; Indels
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                               Score
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   PIR_80:*
1: pir1:*
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Match
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Gapop 10.0 ,
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38
1 RALPSPP 7
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  Copyright
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  GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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 T02081
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C64946
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Bassoon protein -
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Query Match 92.1%; Score 35; DB 2; Length 218; Best Local Similarity 85.7%; Pred. No. 45; Matches 6; Conservative 1; Mismatches 0; Indels	RESULT 2 C64946 C64946 hypothetical protein b1843 - Escherichia coli (strain K-12) C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul C;Accession: C64946 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: C64946 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-218 <blat' a;cross-references:="" a;experimental="" b1843<="" c;superfamily:="" coli="" escherichia="" gb:ae000278="" hypothetical="" k-12,="" mg1655="" protein="" source:="" strain="" substrain="" td="" uniparc:upi000013bc61;="" uniprot:p76280;=""><td>1 RALPSPP 7 : 33 RAVPSPP 39</td><td>Match 92.1%; Score 35; DB 2; Length 156; ocal Similarity 85.7%; Pred. No. 31; s 6; Conservative 1; Mismatches 0; Indels</td><td>37 32 84.2 224 2 370315 38 32 84.2 266 2 736096 39 32 84.2 760 2 786387 40 32 84.2 1051 1 JW0051 41 32 84.2 1133 2 715529 42 32 84.2 1133 2 715529 44 32 84.2 133 2 A37488 43 32 84.2 133 2 A37488 44 32 84.2 133 2 A75540 RESULT 1 737009 Appothetical protein SCJ11.38c - Streptomyces coelicolor C; pacies: Streptomyces coelicolor C; pacies: Streptomyces coelicolor C; pacies: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change OC; pate: O3-Dec-1</td></blat'>	1 RALPSPP 7 : 33 RAVPSPP 39	Match 92.1%; Score 35; DB 2; Length 156; ocal Similarity 85.7%; Pred. No. 31; s 6; Conservative 1; Mismatches 0; Indels	37 32 84.2 224 2 370315 38 32 84.2 266 2 736096 39 32 84.2 760 2 786387 40 32 84.2 1051 1 JW0051 41 32 84.2 1133 2 715529 42 32 84.2 1133 2 715529 44 32 84.2 133 2 A37488 43 32 84.2 133 2 A37488 44 32 84.2 133 2 A75540 RESULT 1 737009 Appothetical protein SCJ11.38c - Streptomyces coelicolor C; pacies: Streptomyces coelicolor C; pacies: Streptomyces coelicolor C; pacies: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change OC; pate: O3-Dec-1
18; s 0; Gaps 0;	<pre>win K-12) #text_change 09-Jul-2004 prna, N.T.; Burland, V.; Riley, M.; (a coli K-12. 8503 iion not shown 113BC61; GB:AE000278; GB:U00096; NID 55 15 b1843</pre>	, , , ,		nodulin - soybean probable secreted probable pto kinas serine/threonine-s hypothetical prote Ras guanine nucleo Ras guanine nucleo hypothetical prote

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1 RALPSPP 7

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hypothetical protein Z2893 [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli (c;Species: Escherichia coli (c;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: E85796 C;Accession: E85796 Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Marieman, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mailler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-218 <HAY>
A;Cross-references: UNIPROT:QBXCK7; UNIPARC:UPI00000D0475; GB:BA000007; PIDN:BAB35976.1,
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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A99948
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hypothetical protein F8M12.9 - Arabidopsis thaliana ()Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 # C;Accession: T01882 T.; Cotton, M.; Modde, T. submitted to the EMBL Data Library, July 1998 A;Description: The sequence of A. thaliana F8M12.
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A99948
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C;Superfamily: Escherichia coli hypothetical protein b1843
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1; Mismatches
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Biosci. Biotechnol. Biochem. 63, 302-308, 1999
A;Title: Molecular cloning and characterization of a cDNA
A;Reference number: JG0179; MUID:99208990; PMID:10192910
A;Accession: JG0179
A;Accession: JG0179
A;Molecular cloninary
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A;Residnes. **Inc.** **
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A;Rolecule type: DNA
A;Residues: 1-665 <BEV>
A;Residues: 1-665 <BEV>
A;Cross-references: UNIPROT:Q9SN59; UNIPARC:UPI00000AA1C9;
A;Cross-references: Cultivar Columbia; BAC clone F25I24
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A; Residues: 1-649 < M
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A;Status: translated
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C;Species: Oryza sativa (rice)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: JG0179
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A; Introns: 6/2;
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Query Match
Best Local Similarity
"hes 6; Conserve
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nilarity 85.7%;
Conservative
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                         Conservative
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85.7%;
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1; Mismatches
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Pred. No.
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                                                                Score 34;
Pred. No.
                                                             Pred.
                                   Mismatches
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March 1999
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Maria Commenter

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hypothetical protein KIAA0434 - C;Species: Homo sapiens (man) C;Date: 22-Jan-1999 #sequence_re C;Accession: T00062 R;Ishikawa, K.; Nagase, T.; Naka submitted to the EMBL Data Libra
                                                                                                                                                                                                                    RESULT
T00062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R/Gupta, V.K.; Berrhoud, V.M.; Atal, N.; Jarillo, J.A.; Barrio, L.C.; Beyer, Invest. Ophthalmol. Vis. Sci. 35, 3747-3758, 1994

A;Title: Bovine connexin44, a lens gap junction protein: molecular cloning, A;Reference number: I46053; MUID:94375220; PMID:8088962

A;Accession: I46053

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-402 <GUP>
A;Cross-references: UNIPARC:UPI0000177531; EMBL:U08213; NID:g469557; PIDN:AJC;Superfamily: gap junction protein
   A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-1571 <ISH>
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Dialus. F-1.
A; Molecule type: DNA
A; Molecule type: CANA
A; Residues: 1-1222 < KANA
A; Cross-references: UNIPROT: Q9YC75; UNIPARC: UPI000005DF12; DDBJ: AP000061;
A; Cross-references: Strain K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              awa, H.; Takamıya, W., 1999
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic
                                                        A; Accession: T00062
                                                                       A; Reference number:
                                                                                            A; Description:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable reverse gyrase APE1376 - Aeropyrum pernix (strain K1)
(;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72614
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C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 13-Aug-1999
C;Accession: I46053
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Matches 6
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RVLPSPP
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                                                                                            Prediction of
                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                           T.; Nakajima, D.; Seki, N.; Ohira, ata Library, October 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.5%;
85.7%;
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Pred. No. 4.1e
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Pred. No. 1.3e
0; Mismatches
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. 4.1e+02;
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1.3e+02;
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                                                                                                                           M.; Miyajima,
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                                                                                                                          N.; Tanaka,
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Query Match
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Matches 6
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A;Description: may be involved in cytomatrix organization A;Note: component of the presynaptic cytoskeleton C;Keywords: coiled coil; zinc finger
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A;Cross-references: UNIPROT:O88737; UNIPARC:UPI0000029B58;
A;Experimental source: strain 129 SVJ
                                                                                                                                                                                                                                                          R;Dieck, S.; Sanmarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, J. Cell Biol. 142, 499-509, 1998
A;Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively A;Reference number: Z22249; MUID:98345363; PMID:9679147
A;Accession: T42730
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A;Residues: 1-3938 cDIE>
A;Residues: 1-3938 cDIE>
A;Cross-references: UNIPROT:088778; UNIPARC:UPI00000E7EDE;
A;Experimental source: strain Sprague Dawley; brain
C;Function:
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A;Experimental source: brain; clone HH2165
C;Genetics:
                                                             A; Note: bassoon C; Function:
                                                                                                                                                                                                                                                                                                                                                                Bassoon protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42730
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A;Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively A;Reference number: Z22249; MUID:98345363; PMID:9679147
                                                                                                     A; Map position: (A; Introns: 72/2;
                                                                                                                                                                                                                       A; Molecule type: DNA
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A;Status: preliminary; translated
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C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change
C;Accession: T42761
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Pred. No. 1.4e
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O; Mismatches
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5.3e+02;
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Similarity 85. 6; Conservative

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Score 34; DB Pred. No. 1.4e 0; Mismatches

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RALPSPP

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RESULT 13
T46448
                                                                                                                               hypothetical protein DKPZp586J1923.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #text_change 09-Jul-2004
C;Date: 11-Jun-1999 #text_change 09-Jul-2004
C;Datc: 10-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08808
R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
                                                                                                                                                                                                                                                                             RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA- and ripening-inducible-like protein - maize C;Species: Zea mays (maize) C;Species: Zea mays (maize) C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004 C;Accession: T02081 R;Arredondo-Peter, R.; Shearman, L.; Ji, L.; Klucas, R.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q9NTF5; UNIPARC:UPI000006D41B; EMBL:AL137301
A;Experimental source: adult testis; clone DKPZp434N1429
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A;Molecule type: mRNA
A;Residues: 1-135 <AAA>
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A;Accession: T46448
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C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46448
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A;Residues: 1-196 <ANS>
A;Cross-references: UNIPROT:Q9UKR3; UNIPARC:UPI000016AC51; EMBL:AL050220
A;Experimental source: adult uterus; clone DKFZp586J1923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-169 <ARR>
A;Cross-references: UNIPROT:Q41730; UNIPARC:UPI00000A2CC1; EMBL:U09276; NID:g551482; PID
A;Experimental source: strain Golden Bantam; mesophyll
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submitted to the EMBL Data Library, April 1994
A;Description: Nucleotide sequence of an ABA- and ripening-like cDNA isolated from corn
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A; Accession: T02081
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A; Accession: T08808
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C;Superfamily: trypsin; trypsin homology
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ative 0; Mismatches
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Q83VX9 STRCU
Q6ZIV3 ORYSA
Q84LF5 ORYSA
Q94LF5 ORYSA
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Q55ZE2 CRYNE
Q5KZMO MYCSM
Q67UAO ORYSA
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VX9_STRCJ
VX9_STRCJ PRELIMINARY;
Q83VX9_STRCJ PRELIMINARY;
Q83VX9;
01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
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STRAIN=Type strain DSM 40005;

MEDLINE=2558541, PubMed=12642677; DOI=10.1073/pnas.0230516100;

MIDDLINE=2558541, PubMed=12642677; DOI=10.1073/pnas.0230516100;

Widdick D.A., Dodd H.M., Barraille P., White J., Stein T.H.,

Chater K.F., Gasson M.J., Bibb M.J.;

"Cloring and engineering of the cinamoreus cinnamoreus DSM40005.";

Proc. Natl. Acad. Sci. U.S.A. 100:4316-4321(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
Sasaki T., Matsumoto T., Katayose Y.;
Sasaki T. Matsumoto T., Katayose Y.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ
EMBL; AP005245; BAD10187.1; -; Genomic_DNA.
Gramene; Q6Z3R7; -.
                                                                                                                                                                                                                                                                                                                            Streptomyces cinnamoneus.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=53446;
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R7 ORYSA
Q6Z3R7_ORYSA PRELIMINARY;
Q6Z3R7;
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Name=cinR;
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Q8KLKS STRTO
Q5Z8A4 ORYŚA
Q698X7 9BRAS
Q85Z10 BRAJU
Q8LSTO 9BRAS
Q8LSTO 9BRAS
Q8LSTO 9BRAS
Q8LSTO 9BRAS
Q8LSTO ARATH
Q941PO BRAJU
Q9MERO ARATH
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a; Poales; Poaceae;
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                                                                                                                                                                                                                                                        "Oryza sativa nipponbare(GA3) genomic DNA, chrom tolone:OJ1051 A08.";

Submitted (JÜL-2001) to the EMBL/GenBank/DDBJ dat RMBL; AP003947; BAC99436.1; -; Genomic DNA. REMBL; AP003904; BAC99374.1; -; Genomic DNA. R Gramene; QGZIVJ; -.

Hypothetical protein.
SEQUENCE 233 AA; 24114 ***
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GO; GO:0005700; F:transcription factor activity; IEA.
GO; GO:0000156; F:two-component response regulator acti
GO; GO:0000156; F:two-component response regulator acti
GO; GO:000760; P:sensory perception; IEA.
GO; GO:0006350; P:transcription; IEA.
GO; GO:0006350; P:two-component signal transduction sys
GO; GO:0006160; P:two-component signal transduction sys
InterPro; IPR001789; Response_reg.
InterPro; IPR001789; Response_reg.
InterPro; IPR011991; Wing_hlx_DNA_bd.
Pfam; PF00072; Response_reg; 1.
RFANTS; PR00038; HTH_LUXR; 1.
R PRODOM; PD000030; HTH_LUXR; 1.
R PRODOM; PD000030; Response_reg; 1.
R PRODOM; PD000030; Response_reg; 1.
R PRODOM; PD000030; Response_reg; 1.
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R SMART; SM00421; HTH_LUXR; 1.
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IV3 ORYSA
QGZIV3 ORYSA PRELIMINARY;
QGZIV3;
Q5-JUL-2004 (Tremelrel. 27
05-JUL-2004 (Tremelrel. 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation; Two-component regulatory SEQUENCE 216 AA; 22938 MW; 5D1E66581B306AB9 CR
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Submitted (JŪL-2001) to the EMBL/G
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DNA-binding; Sensory transduction; Transcription;
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294LP5 ORYSA
294LP5 ORYSA PRELIMINARY; PRT; 408 AA.

ID 094LP5; Q84MW4;

DT 01-DEC-2001 (TERMBLrel. 19, Created)
DT 10-MAY-2005 (TERMBLrel. 30, Last annotation update)
DT 10-MAY-2005 (TERMBLrel. 30, Last annotation update)
DE Hypothetical protein (Expressed protein).

GN ORYSA Sativa (japonica cultivar-group).

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzaa.
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Q8H2Z5;
01-MAR-2003
01-MAR-2003
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"Oryza sativa nipponbare (GA3) genomic
clone:P0710F09.";
Submitted (MAY 2002) to the EMBL/GenBa
EWBL; AP00535; BAC21552.1; -; Genomic
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Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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           Buell C., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones Overton II L., Tsitrin T., Kim M., Bera J., Jin S., Fadrosh Tallon L., Koo H., Zismann V., Heiao J., Blunt S., Vanaken Riedmiller S., Utterback T., Feldblyum T., Yang Q., Haas B. Peterson J., Quackenbush J., White O., Salzberg S., Fraser Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases. EMBL; AC084295, AAK55468.1; -; Genomic DNA.
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                                                                                                                                          NUCLEOTIDE
Buell C., 1
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Gramene;
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a; Poales; Poaceae;
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Fraser C.;
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W NUCLEOTIDE SEQUENCE.

RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,

RA Chow T.-Y., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,

RA Chao Y.-T., Chang S.-J., Chen G.-I., Han S.-Y., Hsiao S.-H.,

RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,

RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,

RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,

RA Wu H.-P., Shaw J.-F.,

RT "Oryza sativa BAC OJ1123 C08 genomic sequence.";

RI Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AC108875; AAV32132.1; -, Genomic DNA.

DR InterPro; IPR007719; Phytcheltn synth.

Pram. PF05023; Phytochelatin; 1.
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Matches 7
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Wickes
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                                                            Cryptococcus neoformans var. neoformans B-3501A.
Cryptococcus neoformans yar. neoformans B-3501A.
Bukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
NCBI_TaxID=283643;
                                                                                                         ORFNames=CNBA5470;
                                                                                                                                                            Q55ZE2_CRYNE
Q55ZE2;
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25-OCT-2004
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PROSITE; PS50181; FBOX; 1.
                                STRAIN=B-3501A;
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          Hyman R.W., Rowle
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Pred. No. 3.3
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Pred. No. 2.4
); Mismatches
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                                                                                              C STRAIN=JEC21;

PubMed=1553466; DOI=10.1126/science.1103773;

PubMed=1553466; DOI=10.1126/science.1103773;

A Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,

A Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,

A Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,

A BOSDET C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,

A Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,

A Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,

A Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,

A Kwon-Chung K.J., Lengeler K.B., Maiti R., Siggs F.R., Salzberg S.L.,

A Kwon-Chung K.J., Longeler K.B., Maiti R., Shunway M., Specht C.A.,

A Schein J.E., Shvartsbeyn A., Shin H., Shunway M., Specht C.A.,

A Schein J.E., Shvartsbeyn A., Shin H., Shunway M., Specht C.A.,

A Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,

A Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,

Fraser C.M., Hyman R.W.;

The genome of the basidimycetous yeast and human pathogen
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A Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
A Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
A D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fusushina M., Haas B.J.,
A Huang J.C., Janbon G., Jones S.J.M., Krzywinski M.I., Kwon-Chung J.K.
A Lengeler K.B., Maiti R., Marra M.A., Marra R.E., Mathewson C.A.,
A Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L., Shvartsbeyn A.,
A Schein J.E., Shin H., Specht C.A., Suh B., Tenney A., Utterback T.,
A Mickes B.L., Wye N.H., Kronstad J., Lodge J.K., Heitman J.,
Davis R.W., Fraser C.M., Hyman R.W.;
The genome and transcriptome of Cryptococcus neoformans, a
basidiomycete fungal pathogen of humans.";
Science 0:0-0(2005).
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Q5KNQ7_C
                                                     Cryptococcus neoformans."; Science 307:1321-1324(2005).
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Cryptococcus Pungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
NCBI_TaxID=214684;
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
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Van Aken S.,
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J. Bacteriol. 186:4051-4055 (2004)

REMBI; AY205337; AAO43178.1; -; Genomic_DNA.

GO; GO:0005835; C:fatty-acid synthase complex; IEA.

GO; GO:0004312; F:fatty-acid synthase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase.

GO; GO:0006633; P:fatty acid biosynthesis; IEA.

GO; GO:0008152; P:metabolism; IEA.

R Ffam; PF001227; Ac_transferase.

InterPro; IPR000794; Ketoacyl_synth.

R Pfam; PF00109; Acyl_transferase.

R Pfam; PF00109; Ketoacyl-synt; 1.

R Pfam; PF00109; Ketoacyl-synt; C; 1.

R Pfam; PF001575; MaoC dehydratas; 1.

R Pfam; PF02801; Ketoacyl-synt; C; 1.

R Pfam; PF03801; Asgradatas; 1.
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05-JUL-2004 (TrEMBLrel.
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Zimhony O., Vilcheze C., Jacobs W.F.
"Characterization of Mycobacterium
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                                                 Oryza sativa (japonica cultivar-group). Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; Liliopsid: Ehrhartoideae; Oryzaa. NCBI_TaxID=39947;
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25-OCT-2004 (TrEMBLrel. 28, Last
25-OCT-2004 (TrEMBLrel. 28, Last
25-OCT-2004 (TrEMBLrel. 28, Last
Hypothetical protein P0025H07.9.
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Bacteria, Actinobacteria,
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A; 329440 MW; F61433A3A824A\overline{4}0A CRC64;
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Pred. No. 7.9e+02;
                                                                                                                                   Liliopsida;
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                                                                                                                               Embryophyta; Tracheophyta;
a; Poales; Poaceae;
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05-JUL-2004
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Name=P0711H09.20,
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, En
Spermatophyta, Magnoliophyta, Liliopsida,
Ehrhartoidese, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HMBL: AP005655; BAD38271.1; Gramene; 067UA0; -. Hypotherical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Oryza sativa nipponbare clone:P0025H07."; Submitted (AUG-2002) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sasaki T., Matsumoto T., Yam
Submitted (FEB-2002) to the
EMBL, APO04765; BAD10070.1;
Gramene; Q6Z8N1; -.
Hypothetical protein.
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II ORYSA
O6Z8N1 ORYSA PRELIMINARY;
O6Z8N1;
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Sasaki T., Matsumoto
Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E., Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S. Arachchi H., Armbruster J., Barnantsang P., Baldwin J., Barry A. Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L., Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N., Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citro
                                                                                                                                Magnaporthe grisea 70-15.
Eukaryota; Fungi; Ascomycota; Pe
Eukaryota; incertae sedis;
Sordariomycetes incertae sedis;
NCBI_TaxID=242507;
                                                                                                                                                                                            Hypothetical protein. ORFNames=MG01221.4;
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                                                                                                                                                                                                                                                                 Q52GR5 MAGGR PRELIMINARY;
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the EMBL/GenBank/DDBJ
.1; -; Genomic_DNA.
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Pred. No. 5.1e+02;
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                                                                                                                                                 Pezizomycotina; Sordariomycetes; s; Magnaporthaceae; Magnaporthe.
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v
 NUCLEOTIDE SEQUENCE
                                                Viruses; ssDNA viruses;
                                                                                                                                           Q5ENX5_9VIRU
Q5ENX5;
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                          NCBI_TaxID=68887;
                                                              Torque teno virus
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(TrEMBLrel.
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Pred. No.
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l; Mismatches
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                                                                                            sequence update) annotation updat
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                                                                        Q9WQH1 9VIRU PRELIMINARY;
Q9WQH1;
01-NOV-1999 (TYEMBLYE1. 1
01-NOV-1999 (TYEMBLYE1. 1
01-OCT-2003 (TYEMBLYE1. 2
                                                                                                                                                                                                                                                                                                                Sugano S., Gojoboxi T., Shen J.C.-K., Wu C.I., Hashimoto K.; "Substitution rate and structural divergence of 5'UTR evolution: Comparative analysis between human and cynomolgus monkey cDNAs."; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. EMBL; ABIG8214; BAE00339.1; -; mRNA. SEQUENCE 118 an. 157.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2005
13-SEP-2005
13-SEP-2005
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Niel C., Diniz-Mendes L., Devalle S.;
"Rolling-circle amplification of Torque teno virus (T
"Rolling-circle amplification sera and identification
                                        Torque teno virus.
Viruses; ssDNA vir
                                                                                                                                                                                                                                                                                                                                                                                                                                     "DNA sequences of macaque genes expressed in brain or te
evolutionary implications.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Euarchontoglires; Pri
Cercopithecidae; Cercopithecinae; Macaca.
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InterPro; IPR004118; TT_ORF2.
Pfam; PF02957; TT_ORF2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomes from human and swine sera TTV genogroup.";
J. Gen. Virol. 86:1343-1347(2005).
NUCLEOTIDE SEQUENCE
                                                                 Hypothetical protein.
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Chordata; Craniata; Vertebrata; Euteleostomi;
Euarchontoglires; Primates; Catarrhini;
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Search completed: April 4, 2006, 13:15:15
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RA Mushahwar I.K., Erker J.C., Muerhoff A.S., Leary T.P., Simons J.N.,
RB Birkenmeyer L.G., Chalmers M.L., Pilot-Madias T.J., Dexai S.M.;
RT "Molecular and biophysical characterization of TT virus: evidence for a new virus family infecting humans.";
RI Proc. Natl. Acad. Sci. U.S.A. 96:3177-3182(1999).
RI Proc. Natl. Acad. Sci. U.S.A. 96:3177-3182(1999).
RI Proc. Natl. Acad. Sci. U.S.A. 96:3177-3182(1999).
RR PROCLEOTIDE SEQUENCE.
RR MEDLINE=99350006; PubMed=10423143;
RR Erker J.C., Leary T.P., Desai S.M., Chalmers M.L., Mushahwar I.K.;
RT "Analyses of TT virus full-length genomic sequences.";
J. Gen. Virol. 80:1743-1750(1999).
RR EMBL; AF122914; AAD44680.1; -; Genomic_DNA.
DR InterPro; 1PR004118; TT_ORF2.
DR Ffam; PP02957; TT_ORF2: 1.
RW Hypothetical protein.
SQ SEQUENCE 150 AA; 15621 MW; 43271527702CFE94 CRC64;
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

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1 RALPSPP 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration
    2 US-09-428-082B-293
2 US-08-602-999A-78
2 US-08-278-865-78
2 US-09-238-315-78
2 US-09-38-315-78
2 US-09-938-315-78
2 US-09-938-315-78
2 US-09-938-315-78
2 US-09-938-315-78
2 US-09-938-315-78
2 US-09-95-99A-45
2 US-09-95-99A-16784
2 US-09-902-540-13693
2 US-09-902-540-13693
2 US-09-902-16-7708
2 US-09-34-123-2
2 US-09-949-016-7708
3 US-09-949-016-7708
3 US-09-95-16-7708
3 US-09-95-16-7708
3 US-09-252-991A-303
3 US-09-252-991A
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651.178 Million cell updates/sec
Sequence 293, App
Sequence 78, Appl
Sequence 78, Appl
Sequence 78, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 16784, A
Sequence 13693, A
Sequence 2, Appl
Sequence 2708, Ap
Sequence 333, App
Sequence 31248, A
Sequence 12, Appl
Sequence 12, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 35, Appl
Sequence 35591, A
Sequence 61654, A
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33 86.8 135 2 US-09-199-637A-217 33 86.8 167 2 US-09-270-7677-45418 33 86.8 167 2 US-09-2949-016-10516 33 86.8 173 2 US-09-252-991A-19768 33 86.8 189 2 US-09-252-991A-19341 33 86.8 224 2 US-09-252-991A-19341 33 86.8 229 2 US-09-199-016-8166 33 86.8 329 2 US-09-199-637A-311 33 86.8 351 2 US-09-199-637A-311 33 86.8 351 2 US-09-245-041-11 33 86.8 351 2 US-09-358-055B-11 33 86.8 351 2 US-09-358-025B-11 33 86.8 351 2 US-09-358-035B-11 33 86.8 351 2 US-09-252-991A-30849 33 86.8 369 1 US-08-230-047-5 33 86.8 394 2 US-09-252-991A-30849 33 86.8 440 2 US-09-252-991A-30849 33 86.8 440 2 US-09-252-991A-30849 33 86.8 440 2 US-09-252-991A-30849 34 86.8 459 2 US-09-252-991A-24229 35 86.8 459 2 US-09-252-991A-24229
. 8 163 2 US-09-297-767-45418 . 8 167 2 US-09-290-7076-745418 . 8 169 2 US-09-292-991A-1976 . 8 1189 2 US-09-252-991A-2496 . 8 129 2 US-09-252-991A-2496 . 8 224 2 US-09-252-991A-2496 . 8 229 2 US-09-199-637A-341 . 8 351 2 US-09-245-041-11 . 8 351 2 US-09-245-041-11 . 8 351 2 US-09-245-047-5 . 8 369 1 US-09-252-991A-2084 . 8 369 1 US-09-252-991A-2084 . 8 369 2 US-09-252-991A-2084 . 8 388 2 US-09-252-991A-2084 . 8 394 2 US-09-252-991A-2084
2 US-09-19-637A-217 2 US-09-270-767-45418 2 US-09-270-767-4518 2 US-09-270-767-4518 2 US-09-252-991A-1934 2 US-09-252-991A-246 2 US-09-252-991A-246 2 US-09-19-637A-341 2 US-09-245-041-11 2 US-09-245-041-1 2 US-09-245-047-5 2 US-09-252-991A-277 2 US-09-252-991A-277 2 US-09-252-991A-2422 2 US-09-252-991A-2422
US-09-199-637A-217 US-09-270-767-45418 US-09-270-767-45418 US-09-252-991A-1976 US-09-252-991A-2469 US-09-252-991A-2469 US-09-252-991A-341 US-09-199-637A-341 US-09-199-637A-341 US-09-199-238-11 US-09-193-238-11 US-09-252-991A-2012 US-09-252-991A-2777 US-09-252-991A-2777 US-09-830-230A-93 US-09-252-991A-2122
-09-19-637A-217 -09-270-767-45418 -09-949-016-10516 -09-945-91A-1934 -09-252-991A-1944 -09-252-991A-2466 -09-199-637A-341 -09-245-041-11 -09-348-041-1 -09-328-058-11 -09-252-991A-277 -09-252-991A-2777 -09-252-991A-2777 -09-252-991A-2777 -09-252-991A-2777 -09-252-991A-2777 -09-252-991A-2777 -09-252-991A-2422

ALIGNMENTS

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APPLICANT: FRIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHESTHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THER
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: Patentin version 3.1
SEQ ID NO 293
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
COMMENT THOROGOMATTION: SHY ANTAGONIST DEPTIDE
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: OUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND ME'
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
"hehes 7; Conserva
                                                                                                                                                                                                                                                                                       RESULT 2
US-08-602-999A-78
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US-09-428-082B-293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: SH3 ANTAGONIST PEPTIDE US-09-428-082B-293
                                                                                                                                                                                                                                               Sequence 78, Application US/08602999A Patent No. 6184205
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GENERAL INFORMATION:
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1 RALPSPP 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 38; DB 2; 100.0%; Pred. No. 4.6e+05
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US-08-278-865-78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: KAY, BRIAN K.

APPLICANT: SPARKS, ANDREW B.

APPLICANT: THORN, JUDITH M.

APPLICANT: QUILLIAM, LAWRENCE A.

APPLICANT: DER, CHANNING J.

TITLE OF INVENTION: STC SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: 150LATING AND USING SAME NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC Compatible
COMPUTER: LEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
LS/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PROPERS PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/278,865
ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                       STREET: 1755 S. Jefferson Davis Highway, Suite 400 CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
                                                                       CLASSIFICATION:
                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
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1155 Avenue of the Americas
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SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOG: unknown
MOLECULE TYPE: peptide
US-08-278-865-78
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                                                                        US-09-500-124-78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 78:
Query Match
                                                                                                                                                                                                                                                                                                                                                                             NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18872
REFERENCE/DOCKET NUMBER: 1101-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                 TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FORM:
COMPUTER: PC-DOS/MS-DOS
COMPUTER:
COMPUTER: PC-DOS/MS-DOS
COMPUTER:
COMPU
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APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 100.0%; Score 38; DB Local Similarity 100.0%; Pred. No. 2.1; nes 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 RALPSPP 10
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                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                     13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DER, Channing J. FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QUILLIAM, Lawrence A.
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THORN, Judith M.
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        100.0%;
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        Score 38;
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            DB 2;
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            Length 13;
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Pred. No. 2.1; ; Mismatches

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Best Local Similarity

Contact project

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US-08-278-865-45
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US-09-938-315-78
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                                                                                                                                                                                                                                                                                                                                                 US-09-938-315-78
GENERAL INFORMATION:
APPLICANT: KAY, BR:
APPLICANT: SPARKS,
APPLICANT: THORN, C
APPLICANT: QUILLIAN
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEFAX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 78, Application Patent No. 6703482
GENERAL INFORMATION:
                                                                                       Sequence 45, Application US/08278865
Patent No. 6303574
                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,315
FILING DATE: 23-Aug-2001
CLASSIFICATION: CUnknown>
                                                                                                                                                                                                                                                                         Local Similarity
ses 7; Conserv
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 78:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KAY, BRIAN K.
SPARKS, ANDREW B
THORN, JUDITH M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 4980-007-0 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \widetilde{\text{DER}}_{i}, CHANNING J. TITLE OF INVENTION: SIC SH3 BINDING PEPTIDES AND METHODS ISOLATING AND USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 106 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       1 RALPSPP 7
                                                                                                                                                                                                   RALPSPP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Villacorta, Gilberto M. REGISTRATION NUMBER: 34,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1755 S. Jefferson Davis Highway, Suite 400 CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RALPSPP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09938315
KAY, BRIAN K.
SPARKS, ANDREW B.
THORN, JUDITH M.
QUILLIAM, LAWRENCE !
                                                                                                                                                                                                                                                                         Conservative
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Pred. No.
                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                          2.1;
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; MOLECULE TYPE: peptide
US-08-278-865-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                                                                                                                                                                                           Sequence 45, Application Patent No. 6703482
GENERAL INFORMATION:
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TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 45
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,865
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DER, CHA
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980-007-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Ariington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        DER, CHANNING J.

TITLE OF INVENTION: Src SH3 BINDING PEPTIDES AND METHODS OF ISOLATING AND USING SAME
                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                               STREET: 1755 S. CITY: Arlington STATE: Virginia COUNTRY: U.S.A. ZIP: 22202
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                                                                                                                                                                                                    ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09938315
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VENTION: Src SH3 BINDING PEPTIDES
VENTION: ISOLATING AND USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OBLON,
                                                                                                                                                                                                                                                                                                                                                               KAY,
                                                                                                                                                                                                                                                                                                         SPARKS, ANDREW B.
THORN, JUDITH M.
QUILLIAM, LAWRENCE A.
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                                                                                                                                                                   Jefferson
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Pred. No.
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                                                                                                                                                                   Davis Highway, Suite 400
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                Version #1.25
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TOPOLOGY: unknown

HOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-938-315-45
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Best Local S
Matches 7
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NAME: Villacorta, Gilberto M.

REGISTRATION NUMBER: 34,038

REFERENCE/DOCKET NUMBER: 4980-007-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEPAX: (703) 413-220

TELEPAX: (703) 413-220

TELEPAX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 45, Application US/08602999A Patent No. 6184205
                                             TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A. ZIP: 10036-2711
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FILING DATE: 23-Aug-2001
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 25 amino acids
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26 amino acids
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RESULT 9
US-09-500-124-45
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                                               Query Match
Best Local Similarity
7; Conserva
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                                                                                                                                 ; MOLECULE TYPE: peptide US-09-500-124-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45, Application US/09500124 Patent No. 6432920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Sest Local Similarity 100.0%; Figure 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: SPARKS,
                                                                                                                                                                                                                                      TELEPHONE: (212) 790-5
TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/6(
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 10036-2711
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                                                                                                                                                                      TOPOLOGY:
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13 RALPSPP 19
                              1 RALPSPP 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1155 Avenue of the Americas
                                                              100.0%; Score 38; DB 2;
ilarity 100.0%; Pred. No. 4.3;
Conservative 0; Mismatches C
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                                                                                                                                                                      unknown
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AER: 1101-202
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Pred. No. 4.3;
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RESULT 10 US-09-252-991A-16784

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GENERAL INFORMATION:
APPLICANT: Butler, Karlene H.
APPLICANT: Butler, Comolayo O.
APPLICANT: Harvell, Leslie T.
APPLICANT: Horzeo, Jr., Emil M.
APPLICANT: Rasco-Gaunt, Sonriza
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: Phytochelatin Synthase
FILE REFERENCE: BB1511 US NA
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US-10-214-269-20
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PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 13693
LENGTH: 2000-07-10
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US-09-252-991A-16784
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16784
LENGTH: 204
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APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                            Sequence 20, Appli
Patent No. 6844485
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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                                                                                                                                                                                                                                                                                               151 RALPAPP 157
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BER: US 60/074,788
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85.7%;
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85.7%;
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Pred. No. 1.5e+02;
1; Mismatches 0
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Pred. No. 1.1e+02;
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                                                                                                         Sequence 7708, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOW
TITLE OF INVENTION: WITH HUMAN DISEASE,
FILE REFERENCE: CL001307
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APPLICANT: Rea, Philip
APPLICANT: Vatamaniuk,
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SOFTWARE: Microsoft Office 97
SEQ ID NO 20
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                               CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kim, Eugene J.

APPLICANT: Clemens, Stephan
TITLE OP INVENTION: NOVEL PHYTOCHELATIN SYNTHASES AND USES THEREFOR
FILE REFERENCE: 9596-102U1/209596.0289
CURRENT FILLING DATE: 1999-07-15
CARLIER APPLICATION NUMBER: 09/315,449
EARLIER APPLICATION NUMBER: 09/315,449
EARLIER FILLING DATE: 1999-05-20
EARLIER FILLING DATE: 1999-05-20
EARLIER FILLING DATE: 1998-08-07
NUMBER: 05/095,624
EARLIER FILLING DATE: 1998-08-07
NUMBER: 05-05-20
EARLIER FILLING DATE: 1998-08-07
NUMBER: 05-05-20
ID NOS: 10
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CURRENT FILING DATE: 2002-08-07
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nes 6; Conserv
APPLICATION NUMBER: 60/237,768 FILING DATE: 2000-10-03
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Schroeder, Julian I.
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85.7%;
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85.7%;
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    Mismatches

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Pred. No.
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Pred. No.
                                                                                                                               KNOWN GENES
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7708
LENGTH: 610
TYPE: PRT
ORGANISM: Human
US-09-949-016-7708
                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MASENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 116,872
REFERENCE/DOCKET NUMBER: 1101-2
REFERENCE/DOCKET NUMBER: 1101-2
RELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELLEFAX: (212) 869-9741/8864
TELLEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 333:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: unknown
MOLECULE TYPE: peptide
US-08-602-999A-333
₽ 8
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APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: FOWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
ADDRESSE: Pennie & Edmonds
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US-08-602-999A-333
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Best Local Similarity 85.7%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                          Query Match 89.5%; Score 34; DB 2; Best Local Similarity 85.7%; Pred. No. 11; Matches 6; Conservative 0; Mismatches
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                                                                  RALPSPP 7
                            RALPGPP 11
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1155 Avenue of the Americas
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Search completed: April 4, 2006, 13:09:43 Job time: 1.88874 secs

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Result
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Maximum
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σ	σ	86.8	φ	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8		86.8	86.8	86.8	86.8	86.8	89.5	89.5	89.5
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Adx90372	Adx66082	Abg04951	Adx66532	Aao07541	Abm40003	Aau43484	Abo68120	Abo78884	Ady23754	Aab46485	Add71587	Abg45166	Abg57404	Aam62850	Aam75663	Aam35773	Abb41972	Adh09515	Adh09514	Adv97847
• •	Plant ful	Novel hun	Plant ful	Human pol	Propionik	Propionib	Pseudomor	Pseudomor	Plant ful	B. lichen	Human uri	Human pep	Human liv	Human bra	Human bor	Peptide #	Peptide #	Human hos	Human hos	Murine pr

ALIGNMENTS

RESULT 1

AAB17238 standard; peptide; 7

A

SH3 antagonist 31-OCT-2000 AAB17238;

peptide sequence SEQ

ID NO:294.

(first entry)

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Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPG; TPO; CTDA; mimetic; II; TNNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin; interleukin; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma;
                                                                                                          Novel
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22-OCT-1999;
                                                                                                 active
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                                                                                                                                                                     (AMGE-) AMGEN
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                                                                                                                                                                                                                                                            WO200024782-A2.
                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                   thrombosis; pharmaceutical.
                                                                                                                              2000-350702/30.
                                                                                               composition of matter comprising an Fc epeptides, useful for treating cancer a
                                                                                                                                                 Liu C,
                                                                                                                                                                     INC.
                                                                                                                                                                                        98US-0105371P
99US-00428082
                                                                                                                                                                                                                      99WO-US025044
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                                                                                                                                                  Boone
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                                                                                                c domain and pharmacologically
and autoimmune diseases.
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The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,

Claim 39; Page 299; 608pp; English.

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RESULT 2
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                                                                                                                                                                                             Novel vehicle-peptide molecule inflammatory and autoimmune dis diabetic retinopathy, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; anaemia; thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erythropoletin, TPO; tumour necrosis factor alpha inhibitor; TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
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antianaemic; anorectic; antiinfertility; haemostatic; dermatological
                               multimers.
cytostatic,
                                                         The present invention describes a vehicle-peptide molecule (I) or its multimers. (I) can have antiinflammatory, antitumour, immunosuppressi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAY-2000; 2000US-00563286
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                                                                                                                                                                                                                                                                                                                                                                   Liu C,
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                                                                                                                                               55;
                                                                                                                                                                                                                                                                                                                                                                   Cheetham JC,
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                                                                                                                                         176pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antagonist peptide SEQ ID NO:294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                               antiinflammatory, ic, antiarthritic,
                                                                                                                                            English
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Pred. No. 2e+
0; Mismatches
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                                                                                                                                                                                                                                                      or its
                                                                                                                                                                                                                                                                                                                                                                   Boone
                                                                                                                                                                                                     multimers useful for treating cancer, rheumatoid arthritis, disorders and infertility.
                                                                                                                                                                                                                                                                                                                                                                   TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fusion; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2e+06;
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                                  antitumour, in antidiabetic,
                                                                                                                                                                                                                                                                                                                                                                   Gudas JM
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                               immunosuppressive, c, ophthalmological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ophthalmological;
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cc prophylactic agent as well as for screening purposes. (I) is useful for cc diagnosing diseases characterised by dysfunction of their associated cc protein of interest, for identifying normal or abnormal proteins of cc interest, as a part of diagnostic kit to detect the presence of their cc proteins of interest in a biological sample. Additionally, (I) is useful cc for treating inflammatory and autoimmune diseases, tumour growth, cancer, cc infertility, and neurological degenerative diseases, tumour growth, cancer, cc red blood cell levels such as anaemia. The TPO-minetic comprising EPO-cc mimetic compounds are useful for treating disorders characterised by low cc red blood cell levels such as anaemia. The TPO-minetic comprising cc compounds are useful for treating conditions that involve an existing cc deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic cc tumour which result in thrombocytopaenia, systemic lupus erythematosus, cc and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777 represent amino acid and nucleic acid sequences used in the exemplification of the present invention
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Best Local :
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cardiovascular; infectious; malignant; neurologic disease; anaemia;
immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
                                                                                                                 New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding regiouseful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuroprotective activities.
                                                                                                                                                                                                                         Heavner GA,
                                                                                                                                                                                                                                                                                                                    24-MAR-2003; 2003WO-US009139
                                                                                                                                                                                                                                                                                                                                                16-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ73385 standard; peptide;
                                                                                                                                                                                                                                                                                      29-MAR-2002; 2002US-0368791P
                                                                                                                                                                                                                                                        (CENZ )
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7; Conserv
                                                                                                                                                                                                                                                        CENTOCOR INC
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Pred. No. 2e+
); Mismatches
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2e+06;
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This invention relates to novel mammalian CDR mimetibodies, specific portions or variants thereof. Specifically, it refers to an antibody fragment where a protein has been inserted into, or replaces a portion of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which

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Best Local S
Matches 7
This invention relates to CHI deleted mimetibodies (and the DNA sequence which encode them), compositions, methods and uses. The invention may be useful for the development of compounds with an immunosuppressive, cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, antibacterial, virucide or fungicide activity. In addition, the discloss sequences may prove useful for gene therapy. The CHI-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell,
                                                                                                                                                                                                                                                                                                                         New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, or neurodegenerative disease or disorder, anemia, cancer, or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; IGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ligand binding region (LBR). The present invention describes human mimetibodies, including modified immunoglobulins and cleavage products that can be useful in gene therapy and the generation of transgenic plants and animals. Furthermore, the CDR mimetibody is useful for preparing compositions for modulating, treating or reducing the symptoms of immune, cardiovascular, infectious, malignant and/ or neurologic diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, cardiotatic, antimicrobial, cytostatic and neuroprotective activities. This peptide sequence is an SH3 antagonist peptide sequence used to make a mimetibody of the invention.
                                                                                                                                                                                                                                          Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUN-2002; 2002US-0392431P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUN-2003; 2003WO-US020347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kutoloski
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          multiple sclerosis; dementia; Alzheimer's disease; anaemia; cancerous condition; infectious disease; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CH1 deleted mimetibody-related peptide SeqID840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CENZ ) CENTOCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypotensive; neuroprotective; nootropic; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fungicide; gene therapy; immune disorder; cardiovascular di
arrhythmia; hypertension; heart failure; neurodegenerative;
                                                                                                                                                                                                                                                                                                                                                                                                                                            2004-082870/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection;
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                                                                                                                                                                                                                                          QES
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                                                                                                                                                                                                                                    ID NO 840; 129pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Knight DM,
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Pred. No.
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                                                                                       New CH1 deleted mimetibody polypeptide and nucleic acid, useful diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic
                                                                                  diagnosing, preventing or treendocrine, gastrointestinal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue, organ or animal, specifically for modulating, treating, alleviating, preventing the incidence or reducing the symptoms of an immune, cardiovascular (for example arrhythmia, hypertension or heart failure), or neurodegenerative (for example multiple sclerosis, dementia or Alzheimer's diseases) diseases or disorders, anaemia, cancerous conditions, or infectious diseases (for example bacterial, viral or fungal infection). The present sequence is that of a peptide which may be
                                                                                                                                                                                                                                                                                                            30-JUN-2003; 2003WO-US020495
                                                                                                                                                                                                                                                               28-JUN-2002;
19-SEP-2002;
                                                                                                                                                                                                                                                                                                                                             08-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                          WO2004002424-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                       renal disorder; pulmonary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADJ51980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADJ51980 standard; peptide; 7
                                                                                                                                                        2004-082872/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            during the creation of a mimetibody of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mimetibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mimetibody-related peptide SeqID840.
                                                                                                                                                                                                                                                               2002US-0392431P
2002US-0412144P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                    Knight DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             osteopathic; cardiovascular-Gen;
                                                                                                                                                                                                    Ghrayeb
                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                    Scallon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 8;
2e+06;
                                                                                                                                                                                                    띵,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                        for
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This invention relates to CH1 deleted mimetibodies (and which encode them), compositions, methods and uses. The

the DNA se

DNA sequences ention may be

Claim

15;

SEQ

IJ 8 840;

123pp; English

neurologic

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RESULT 6
AAW11122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastrointestinal-Gen, gymaecological-Gen, hepatotropic, haemostatic, cimmunomodulator, antiallergic, muscular-Gen, cytostatic, antiinflammatory, neuroleptic, ophthalmological, nephrotropic or respiratory-Gen activity acting as a tumour necrosis factor (TNF)-Condulator or cytokine-agonist. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of the CH1 deleted mimetibody, such as a bone or joint, cardiovascular, dental or oral, dermatological, ear, nose or throat, cendocrine, metabolic, gastrointestinal, gynaecological, hepatic, obstetric, heematologic, immunological, allergic, infectious, musculoskeletal, oncological, neurological, nutritional, ophthalmologic, pediatric, psychiatric, renal or pulmonary disorders. The present generate is that of a peptide which may be used during the creation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                     AAW11098-W11124 are peptides that bind to the Src SH3 domain. The SH3 binding peptides are useful in modulating signal transduction pathways the cellular level (especially protein tyrosine kinase-mediated), modulating oncogenic protein activity, or providing compounds for the development of drugs with the ability to modulate broad classes, as well as specific classes, of proteins involved in signal transduction and all the specific classes.
                                                                                                                                                                                                                                                    Peptide with binding affinity for Src proteins - useful for e.g. modulating cellular level, esp. protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
protein tyrosine kinase; signal transduction; RNA processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Src
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW11122 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW11122
                                                                                                                                                                                                       Claim 40; Page 84; 116pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUL-1994;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-FEB-1996
                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-117151/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SH3
regulating the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _
                                                                                                                                                                                                                                                                                                                                                                                                               AΒ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                            Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-00278865.
95US-00483555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95WO-US009382
                                                                                                                                                                                                                                                                                                                                                                                                         BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide; 13
     processing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                            Thorn JM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38;
Pred. No.
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     trafficking or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               Quilliam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in signal transduction
                                                                                                                                                                                                                                                      homology region 3 (SH3) domains of signal transduction pathways at the kinase-mediated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2e+06;
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       translation
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                               and also
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31 _ Matches

Similarity 7, Conserv

Conservative

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 Query Match
Best Local
                                                          AAW16924-W16948 are random recombinant peptides derived from one of three peptide libraries, T9, T12 and R8C. The peptides are all SH3 domain-binding peptides. SH3 binding peptides are useful in modulating signal transduction pathways at the cellular level (especially protein tyrosine kinase-mediated), modulating oncogenic protein activity, or providing compounds for the development of drugs with the ability to modulate broad classes, as well as specific classes, of proteins involved in signal transduction and also for regulating the processing, trafficking or translation of RNA. Conjugates of the peptides with detectable labels or imaging agents are useful for imaging cells, tissues and organs in which src or Src-related proteins are expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conjugates of the peptides with detectable labels or imaging agents are useful for imaging cells, tissues and organs in which Src or Src-related proteins are expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                src; SH3; Src homology region 3; binding affinity; oncogenic
protein tyrosine kinase; signal transduction; RNA processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13
                                                                                                                                                                                                                                            Peptide with binding affinity for Src homology region 3 (SH3) domains proteins - useful for e.g. modulating signal transduction pathways at cellular level, esp. protein tyrosine kinase-mediated.
                                                                                                                                                                                                                                                                                                                                                                             22-JUL-1994;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trafficking;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW16934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW16934 standard; peptide; 45
                                      Sequence 45
                                                                                                                                                                                                                    Disclosure; Fig 1; 116pp; English.
                                                                                                                                                                                                                                                                                                                          Sparks
                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                     (UYNC-) UNIV NORTH
                                                                                                                                                                                                                                                                                                                          AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRLPRTP 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                           Kay
                                        AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation.
                                                                                                                                                                                                                                                                                                                                                                             94US-00278865.
95US-00483555.
                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-US009382
                                                                                                                                                                                                                                                                                                                           BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SH3
                                                                                                                                                                                                                                                                                                                                                     CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                           Thorn JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB
Pred. No. 5.4
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding
  Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                           Quilliam LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide
              DB
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                Length 45;
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RESULT 9
AAU63824
                                                                                                                                                                                  RESULT 8
AAW25497
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                                                                                                                                                                                                        The present sequence represents a random peptide recombinant isolated by the method of the present invention. SH3 (Src homology region 3) binding peptides are selected from: (a) peptides which bind the SH3 domain of peptides which bind the SH3 domain of Nck; (c) peptides which bind the SH3 domain of Nck; (c) peptides which bind the SH3 domain of PhC gamma; (f) peptides which bind the SH3 domain of PhC gamma; (f) peptides which bind the SH3 domain of PhC gamma; (f) peptides which bind the SH3 domain of STC gamma; (f) peptides which bind the SH3 domain of Yes; and (i) peptides which bind the sH3 domain of Yes; and (i) peptides which bind the sH3 domain of Yes; and (i) peptides which bind the sH3 domain of Yes; and (i) peptides can be used in the method to identify inhibitors of their binding to their respective SH3 domain, which could be used to modulate the pharmacological activity of proteins or polypeptide containing the SH3 domain. The peptides can also be used to activate Src or Src-related protein tyrosine kinases, to stimulate the immune response by increasing the production of certain lymphokines, e.g. conjugated molecule to certain cellular compartments containing Src or Src related proteins
                                                                                                                      Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 5; 131pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Src homology region 3 binding peptide - used to activate Src tyrosine kinase(s) and to stimulate immune response by increasing production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cortactin; SH3 domain; binding peptide; Src homology region 3; tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Random peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-424972/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sparks AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW25497 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYNC-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CYTO-)
                                                            31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 אי אייט רט פרושעומדפ immune response
lymphokine(s), e.g. interleukin-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOGEN CORP.
UNIV NORTH CAROLINA.
                                                                                                                       Similarity 7; Conserv
                                                                                                                                                                                 45
                                                              RRLPRTP 37
                                                                                       RRLPRTP 7
                                                                                                                                                                                 ₽
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kay BK,
                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-US002298
                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thorn JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone T9.SRC3.1.
                                                                                                                      0,
                                                                                                                                    Score 38;
Pred. No.
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                                                                                                                       Mismatches
                                                                                                                                  DB 2;
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                                                                                                                                                 presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (BLISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                             polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-2000; 2000US-0199047P
02-JUN-2000; 2000US-0208841P
07-JUL-2000; 2000US-0216747P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful
                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAU39105-AAU68017 represent Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 25019; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS59636.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-2001; 2001WO-US012865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dermatological;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
 1 RRLPRTP 7
                                    7;
                                                      Similarity
                                                                                                        269
                                  100.0%; ilarity 100.0%; Conservative 0;
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/e J, Zhang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitcham JL, Wang S
Jen S, Carter D;
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                                                    Score 38;
Pred. No.
                                    red. No. 80;
Mismatches
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ABM60343

standard;

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                                                                                                                                                                       cc encoding a Propionibacterium acnes protein. The invention also relates to college polypeptides encoded by the polypucleotides (ABM35624-ABM6436) and to clammunogenic fragments of P. acnes polypeptides. The invention and to cadditionally encompasses expression vectors and host cells comprising a comprising a polypeptide of the invention; fusion proteins comprising a polypeptide of the invention; a comprising proteins proteins of the comprising relations or across the polypeptide of the invention; a complete the invention; a comprising relations or across in a complete the proteins of proteins or cells prepared comprising proteins. The polypeptides, fusion proteins, and a method is a vaccine composition (comprising P. acnes in a companied proteins and a method for inhibiting the presence of P. acnes in a companied proteins. The proteins polypeptides, polypucleotides, antibodies, fusion proteins. The proteins or antigen-presenting cells that express the polypeptides are useful for inhibiting the development of P. acnes in a companied proteins. The polymucleotides are natigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acnes composition. The polymucleotides can also be used as probes or primers for composition of an immune response specific for a P. acnes composition is useful for the composition is useful for the primated proteins. The present composition assay. The present composition of an immune response or for treating acne, and the kit is useful for performing a diagnostic assay. The present composition when the primated specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences
                                                                         Matches
                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes predicted ORF-encoded polypeptide #25019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; SEQ ID NO 25019; 1481pp; English
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                                  RRLPRTP 7
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Vallieve-Douglass
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ng S, Jen S,
                                                                       Conservative
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                                                                                          100.0%;
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Lodes MJ,
188 J;
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                                                                         Score 38; DE
Pred. No. 80;
D; Mismatches
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Benson DR,
                                                                                            80;
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                                                                                                           Length 269;
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cc encoding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated containing the polypeptide or its fragment whose expression is inhibited by the containing the polypeptide; (6) inhibited by the containing the polypeptide; (6) inhibited by the containing the polypeptide; (6) inhibiting cellular containing the polypeptide; (6) inhibiting cellular proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway contained for proliferation, or that inhibits cellular proliferation; (8) contained for proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound station of an organism activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent contains; or (13) identifying the target of a compound that inhibits the contains; or (13) identifying the target of a compound that inhibits the contains; or (13) identifying the target of a compound that inhibits the contains; or (13) identifying the target of a compound that inhibits the containing proteins or screening for homologous nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational containing the proliferation of an organism. The antiense nucleic acids are useful for cellular proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target provision of the printed specification, but was obtained in electronic format directly from WIPO at
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06-SEP-2001; 2001US-00948993

25-OCT-2001; 2001US-0342923P

08-FEB-2002; 2002US-00072851

06-MAR-2002; 2002US-0362699P
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Wall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID NO 64454; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2002; 2002WO-US009107
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Trawick
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Carr G
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Forsyth
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Xu HH;
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RESULT 12
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AD ABUJ4594
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CC (1) a vector comprising a promoter operably linked to the nucleic acid (2) a host cell containing the vector; (3) an isolated converse acid; (2) a host cell containing the vector; (3) an isolated collect acid; (2) a host cell containing the vector; (3) an isolated collect acid; (4) an antibody capable of specifically binding conting the polypeptide; (5) producing the polypeptide; (6) inhibited by the containing the polypeptide; (7) identifying a compound that influences the activity of the polypeptide; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway contained for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or agene on which the test compound that inhibits proliferation of an compound; activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound that inhibits proliferation of the strains; or (13) identifying the target of a compound that inhibits the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2001;
06-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium bovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein encoded
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRLPRTP 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 62518; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 2001US-00815242.
; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
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Carr G
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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Xu HH;
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RESULT 1:
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                                                                                                                                                                                    Miao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                    (MIAO/)
(BRIA/)
(BALT/)
                                                                                                                                                                                                                                                            17-OCT-2000; 2000US-0240879P
28-FEB-2001; 2001US-0272207P
06-AUG-2001; 2001US-0310385P
                                                                                                                                                              WPI; 2002-599794/64.
                                                                                                                                                                                                                                                                                                          17-OCT-2001; 2001WO-US032354.
                                                                                                                                                                                                                                                                                                                                 01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                      WO200259322-A2
                                                                                                                                                                                                                                                                                                                                                                            Streptomyces roseosporus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S. roseosporus
                                                                                                                                                                                                                                                                                                                                                                                                           anti-cholesterolemic;
                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                               fungicide; virucide; antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Daptomycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP62761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 295 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                          (SILV/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proliferation of an organism. The antisense nucleic acids are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                    VPW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 RRLPRTP 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RRLPRTP 7
                                                                                                                                                                                                                                         MIAO V P W.
                                                                                                                                                                                                                              BRIAN
                                                                                                                                                                                                          SILVA
                                                                                                                                                                                                                    BALTZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                   Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                           biosynthetic gene cluster;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 daptomycin non-ribosomal peptide synthetase DptA.
                                                                                                                                                                                                          <u>ب</u> ب
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 5754 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
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                                                                                                                                                                                    Baltz
                                                                                                                                                                                                                                                                                                                                                                                                           agrochemical; non-ribosomal peptide synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                     antimitotic; immunomodulatory; siderophore;
                                                                                                                                                                                   쮸,
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Pred. No.
                                                                                                                                                                                    Silva
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                                                                                                                                                                                                                                                                                                                                                                                                                                immunomodulator; antilipemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                           thioesterase; antibacterial;
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87;
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The invention relates to a novel isolated nucleic acid molecule comprising a sequence that encodes a thioesterase or thioesterase domain derived from a bacterial daptomycin biosynthetic gene cluster. The proteins of the invention have antibacterial, fungicide, virucide, antiparasitic, immunomodulator, antilipenic, and cycostatic activity. The polynucleotides may have a use in gene therapy. The compositions and methods of the present invention are useful for generating novel linear and cyclic peptides and improving yield of a product in a cell expressing the present invention are useful for generating novel.

Isolated nucleic acid molecule from a bacterial daptomycin biosynthetic gene cluster encoding a thioesterase or thioesterase domain, useful for generating novel linear and cyclic peptides, and products in a cell.

Claim 25;

Page 166-169; 227pp; English.

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Best Local S
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17-OCT-2001;
10-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           compounds or in producing new compounds, such as antibiotics, antifungals, antivirals, antiparasitics, antimitotics, antifungals, antivirals, anticholesterolemic agents, siderophores, immunomodulatory agents, anti-cholesterolemic agents, siderophores, agrochemicals and cytostatics. The sequence represents a S. roseosporus daptomycin non-ribosomal peptide synthetase of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibacterial; gene therapy; daptomycin biosynthesis gene cluster; daptomycin non-ribosomal peptide synthetase; DptBC; gram-positive bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                   the Streptomyces roseosporus daptomycin biosynthesis gene cluster, especially a daptomycin non-ribosomal peptide synthetase (NRPS) or its subunit, where the (NA) molecule encodes DptBC, and is not pRHHI59. The methods and compositions of the present invention are useful for treatment of a gram-positive bacterial infection of any organ or tissue in the body, including skeletal muscle, skin, bloodstream, kidneys, heart, lung and bone. This sequence represents the daptomycin biosynthesis protein DptA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces roseosporus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-2004
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                                                                                                                                                                                                                                                                             New isolated nucleic acid molecule encoding a daptomycin non-ribosomal peptide synthetase, useful for treatment of a gram-positive bacterial infection of skeletal muscle, skin, bloodstream, kidneys, heart, lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-2002; 2002WO-US024310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003014297-A2
                                                          Sequence
                                                                                                                                                                                                        The invention relates to new isolated nucleic acid (NA) molecules from
                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 9; 292pp; English
                                                                                                                                                                                                                                                                                                                                                                                                            (CUBI-) CUBIST PHARM
 Local Similarity hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    daptomycin non-ribosomal peptide synthetase (NRPS) to be used
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                                                                                                                                                                                                                                                                                                                                                    2003-268192/26.
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100.0%; ilarity 100.0%; Conservative 0
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2001WO-US032354.
2002US-0379866P.
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                                                                                                                                                                                                                                                                                                                                                                               Baltz RH,
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  Score 38; DB
Pred. No. 1.2
0; Mismatches
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Pred. No. 1.2e+03;
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                1.2e+03;
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                             Length 5830;
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                                                                                                                                                          The invention relates to Pseudomonas aeruginosa polypeptides and the complynucleotides encoding them. The sequences are useful in diagnosics and conditions, as molecular targets for diagnostics, complynavis and treatment of pathological conditions resulting from a compound, such as a polypeptide, compound, such as components of compound, as components of components of components of components for acruginosa drugs, as targets for antibacterial drugs, as targets for antibacterial drugs, as target components for diagnosis and/or treatment of p. aeruginosa-caused components for diagnosis and/or treatment of p. aeruginosa-caused components for diagnosis and/or treatment of p. aeruginosa caused components for diagnosis and/or treatment of p. aeruginosa caused components for diagnosis and/or treatment of p. aeruginosa sequences ABO67826-CC ABO84396 represent p. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed components for actions but was obtained in electronic format from USPTO at segulata.uspto.gov/sequence.html
                                                                   Matches
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa polypeptide #4936.
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                                                                                                                                  Sequence 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 21507; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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27-JUL-1998;
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2.1e+02;
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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A70669
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D70809

C708able pabC protein - Mycobacterium tuberculosis (strain H37RV)

C75pecies: Mycobacterium tuberculosis

C75pecies: 
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A;Authors: Sqares, J. Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70809
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T24230
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A; Residues: 1-289 < COL>
                                                                                    C;Genetics:
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Best Local S
Matches 7
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shown

genom

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T13468	T13473	AG1911	JC5759	JDVLVH	G75561	A23282	T34887	T04987	B84518	H72607	E83506	T29421	D70955	T41524	T03844
_	DNA-directed DNA p	hypothetical prote	brain-specific ser	DNA-directed DNA p	ABC transporter, A	RAD52 protein - ye	probable transposa		hypothetical prote	hypothetical prote	probable MFS trans	hypothetical prote	hypothetical prote	rhol gdp-gtp excha	telomerase catalyt

ALIGNMENTS

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hypothetical protein R166.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T24230 R;Matthews, P.
                                      A;Gene: CESP:R166.5
A;Map position: 2
A;Introns: 41/1; 198/1;
                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-761 <WIL-
A;Cross-references: UNIPROT:Q22005; UNIPARC:UPI000007C639; EMBL:Z50795; PIDN:CAA90665.1
A;Experimental source: clone R166
A;Experimental source: clone R166
                                                                                                                                                                                                                            submitted to the EMBL Data A;Reference number: Z19859 A;Accession: T24230
    Query Match
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                                         427/2; 535/2; 613/2; 747/3
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  92.1%; Score 35;
                                                                                                                                                                                                                                                                     Library, August 1995
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Pred. No. 4.5;
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  DB 2;
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hypothetical protein Vng2148h [imported] - Halobacterium sp. NRC-1 C;Species: Halobacterium sp. NRC-1 C;Species: Halobacterium sp. NRC-1 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 C;Accession: A64365
R;MG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; L.A.; Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA-directed RNA polymerase (EC 2.7.7.48) - foxtail RNA-ternate names: 152.3K protein C;Species: foxtail mosaic virus C;Species: foxtail mosaic virus C;Date: 05-Mar-1993 #sequence_revision 05-Mar-1993 #C;Accession: JQ1258 C;Accession: JQ1258 R;Bancroft, J.B.; Rouleau, M.; Johnston, R.; Prins, R;Bancroft, J.B.; Rouleau, M.; Johnston, R.; Prins, T. Con Virol 3, 2002.
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A84365
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A;Residues: 1-1335 <BAN>
A;Residues: 1-1335 <BAN>
A;Cross-references: UNIPROT:P22168; UNIPARC:UPI0000134B1E; GB:M62730; NID:g325391; PIDN:
A;Cross-references: UNIPROT:P22168; UNIPARC:UPI0000134B1E; GB:M62730; NID:g325391; PIDN:
C;Superfamily: eggplant mosaic virus RNA-directed RNA polymerase
C;Keywords: nucleotidyltransferase; RNA biosynthesis
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A,Reference number: E59430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: The entire nucleotide sequence of A; Reference number: JQ1258; MUID:91374015; A; Accession: JQ1258
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Residues: 1-1261 <SAR>
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les 6; Conserv
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         foxtail mosaic virus RNA
PMID:1840610
                                                                                                                                                                                                                                                                                                                                                                                                                DB 80;
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76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1261;
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                                                 Ebhardt, H.; Lowe, T.M.;
                                                                                                          D.W.; Shukla, H.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L.J.; Heldin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G.A.
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                                                                                                            A; Molecule type: DNA
A; Residues: 1-98 < CHE>
          Query Match
Best Local Similarity
                                                                                           Cross-references:
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the nucleotide

UNIPARC: UPI0000137B64; sequence was

137B64; EMBL:X17403; NID:g59591; PIDN:CAA35418.1; submitted to the EMBL Data Library, December 1989

86.8**%**;

Score Pred.

No.

DB 15;

2

Length

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C;Accession: B47447
R;Horne, W.A.; Ellinor, P.T.; Inman, I.; Zhou, M.; Tsien, R.W.;
Proc. Natl. Acad. Sci. U.S.A. 90, 3787-3791, 1993
A;Title: Molecular diversity of Ca(2+) channel alpha 1 subunits
A;Reference number: A47447; MUID:93248175; PMID:7683405
A;Accession: B47447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
B47447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P56698; UNIPARC:UPI0000127266
A;Note: sequence extracted from NCBI backbone (NCBIP:130673)
C;Superfamily: voltage-dependent calcium channel protein alg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references:
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-411 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Discopyge ommata
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change
                                                                                                                                                                                                                                        A;Title: Human cytomegalovirus encodes a glycoprotein homologous A;Reference number: S00661; MUID:88094735; PMID:2827039 A;Accession: S01566
                                                                                                                                                                                                                                                                                                                                                  hypothetical protein - human cytomegalovirus 5
(;Species: human cytomegalovirus, human herpesvirus 5
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
C;Accession: S01566; S09782
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A; Residues: 1-2326 < HOR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene:
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                      A; Reference number: S09749; A; Accession: S09782
                                           Curr. Top. Microbiol. Immunol. 154, 125-169, 1990 A; Title: Analysis of the protein-coding content of the A; Reference number: S09749; MUID:90269039; PMID:2161319
                                                                                                                               A;Cross-references: UNIPROT:P16723; UNIPARC:UP10000137B64; EMBL:Y00293 R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny,
                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-98 <BEC>
                                                                                                                                                                                                                                                                                                          R;Beck, S.; Barrell, B.G.
Nature 331, 269-272, 1988
  A;Status: nucleic
                                                                                                        R;Chee, M.S.; Bankier, A.T.; Beck, M.; Barrell, B.G.
                                                                                                                                                                                                                     A;Status: translation not shown
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acid sequence not shown; translation
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85.7%;
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85.7%;
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Pred. No. 2.2e+02;
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submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn J.D.; Junqueira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr. Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, B.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, C.; de Oliveira, R.C.; Palmieri, D.F. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A,Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A,Reference number: A59328
                                                                                                                                                                                                                   A;Title: Complete genome A;Reference number: A829 A;Accession: H83163
                                                                                                                                                                                                                                                                                                          R;Stover, C.K.; Pham, X.Q.; Erwin, adman, S.; Yuan, Y.; Brody, L.L.; (a., L.Y., S.; Olson, M.V.
                                    C;Superfamily:
                                                         A;Gene: PA3845
                                                                                                       A;Cross-references: UNIPROT:Q9HXG1; UNIPARC:UPI00000C5B3A; A;Experimental source: strain PAO1
                                                                                                                                                       A;Residues: 1-298
                                                                                                                                                                                                     A;Status:
                                                                                                                                                                                                                                                                                         Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 C;Accession: H83163
                                                                                                                                                                                                                                                                                                                                                                                                                                probable transcription regulator PA3845 [imported] -
C;Species: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: for a complete list of authors see reference number A59328 below A;Accession: F82832 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347
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Nature 406, 151-157,
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A; Residues: 1-281 <SIM>
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C;Species: Xylella fastidiosa
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Best Local S
Matches 6
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;Date: 18-Aug-2000 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
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                                 regulatory protein ampR
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                                                                                                                                                                                                                                           enome sequence of Pseudomonas aeruginosa A82950; MUID:20437337; PMID:10984043
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A.; Larbig,
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K.; Li
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                                                                                                                             NID
R;Latreille, P.; Gattung, S. submitted to the EMBL Data Library, April 1996 A;Description: The sequence of C. elegans cosm
                                                                          hypothetical protein K03B6.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #t C;Accession: T34328
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A; Map position: 4
A; Introns: 85/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q05581; UNIPARC:UPI000003064B; GB:L06213; NID:g153219; A;Note: sequence extracted from NCBI backbone (NCBIN:121675, NCBIP:121676) C;Superfamily: clavaminate synthase 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Marsh, B.N.; Chang, M.D.; Townsend, C.A.
Biochemistry 31, 12648-12657, 1992
A;Title: Two isozymes of clavaminate synthase central to
A;Reference number: A44241; MUID:93112607; PMID:1472501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Streptomyces clav
C;Date: 10-Jun-1993 #sequenc
C;Accession: A44241
R;Marsh, E.N.; Chang, M.D.;
                                                                                                                                                                          A;Gene: ATSP:T16L4.240
                                                                                                                                                                                           A;Experimental source: cultivar C;Genetics:
                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q9SU78; UNIPARC:UPI00000A2401; A;Experimental source: cultivar Columbia; BAC clone T16L4
                                                                                                                                                                                                                                                                                 A;Reference number:
A;Accession: T09936
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Best Local :
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Species: Streptomyces clavuligerus
Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
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                                  1 RRLPRTP 7
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RRAPRTP
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Pred. No.
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                                                                                                                                                                                                                              EMBL: AL079344;
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#text_change

09-Jul-2004

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A;Reference number: ?
A;Accession: T34328
A;Status: preliminar;
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule from Expe: DNA
A; Residues: 1-499 < LAT>
A; Cross-references: UNIPROT:Q21194; UNA; Experimental source: strain Bristol C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPARC:UPI0000169030; EMBL:Z54354; NID:g1019398; PIDN:CAA91166.1; R;Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, October 1995
A;Reference number: Z21745
A;Accession: T38567
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T25397
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A;Molecule type: DNA
A;Residues: 1-543 <BAD>
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submitted to the EMBL Data Library,
A;Reference number: S62445
A;Accession: S62456
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-573 <WIL>
                                                    submitted to the EMBL Data Library,
A;Reference number: Z20028
A;Accession: T25397
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                                                                                                                           hypothetical protein T28B11.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te:C;Accession: T25397
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;Experimental source: strain 972h-; cosmid c2G11
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Best Local
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Experimental source: strain Bristol N2; clone K03E6
                                                                                                              ;Kelly,
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b; Pred. No. 75;
0; Mismatches
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Pred. No. 82;
0; Mismatches
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000
C;Accession: G83465
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q22842; UNIPARC:UPI0000079B54; EMBL:Z73977; PIDN:CAA98290.1
A;Experimental source: clone T28B11
C;Genetics:
A;Gene: CESP:T28B11.1
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A;Introns: 32/2; 477/2; 539/1
C;Superfamily: Caenorhabditis elegans hypothetical
                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-650 <STO>
A;Cross-references: UNIPROT:Q913R4; UNIPARC:UPI00000C537B; GB:AE004573; GB:AE004091; NI:
A;Experimental source: strain PAO1
C;Genetics:
                                                                                                                                                                                                                                                                                         A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: G83465
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Search completed: April Job time: 3.14529 secs
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,

A Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,

A Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,

A Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,

A Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,

A Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,

A Holroyd S., Hornsby T., Jagels K., Kselton S., Squares R.,

A Rogers J., Rutter S., Seeger K., Skelton S., Squares R.,

A Rogers J., Rutter S., Seeger K., Skelton S., Squares R.,

A Rogers J., Rutter S., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the

"Complete genome sequence.";

Nature 393:537-544(1998).

"The Complete St. CABS5325.1; -; Genomic DNA.
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Mycobacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;

Woodbacterium tuberculosis complex.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
PROBABLE AMINO ACID AMINOTRANSFERASE (EC 2.6.1.-).
MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100; Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S. Harris B., Akkin R., Doggett J., Mayes R., Keating L., Wheeler P.F. Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; "The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

EMBL; BX248336; CAD93697.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                Q7U179_MYCBO PRELIMINARY; PRT; 289 AA. 07U179; 01-OCT-2003 (TrEMBLrel. 25, Created) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) PROBABLE AMINO ACID AMINOTRANSFERASE (EC 2.6.1.-).
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ProDom; PD001961; Aminotrans IV; 1.
Aminotransferase; Complete proteome;
SEQUENCE 289 AA; 31122 MW; A384C2
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GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
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MEDLINE=22206494; PubMed=12218036;

DOI=10.1128/JB.184.19.5479-5490.2002;

Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O. Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey B.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva I. Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Praser C.M.;
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GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR001544; Aminotrans_IV.
Pfam; PP01063; Aminotran 4; 1.
ProDom; PD001961; Aminotrans_IV; 1.
Aminotransferase; Complete proteome; TransfeseQUENCE 289 AA; 31140 MW; 14A941455727F
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
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Aminotransferase, Class IV.
Name=dat; OrderedLocusNames=MT0833;
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Q8VKD6;
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EMBL; AE000516; AAK45075.1;
TIGR; MT0833; -
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ProDom; PD001961; Aminotrans_IV; 1.
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GO; GO:0008483; F:transaminase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
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ID Q58915 F
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C Eurortial
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RN NUCLEOTI
RC STRAIN-F
RA Birren B
RA Arachchi
RA Grachchi
RA Gardyna
RA Diaz J.
RA Erickson
RA Gardyna
RA Jaffe D.
RA Kells C.
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RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Anthouard V., Jubin C., Cattollco L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Cruaud C., Duprat S., Brottier P., Coutenceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Farra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA Kindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RG "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
Nature 431:946-957 (2004).
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Best Local S
Matches 7
Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S., Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L., Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L., Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J., Choepel Y., Collymore A., Cooke P., Corum B., DeArell Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels I Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N., Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I. Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui
                                                                                                                                                                                                                                                                     Aspergillus nidulans FGSC A4.
Eukaryota; Fungi; Ascomycota;
Eurotiales; Trichocomaceae; Em
NCBI TaxID=227321;
                                                                                                                                                                                                                STRAIN=FGSC
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Eukaryota; Metazoa; Chordata; Craniata; Verte
Actinopterygii; Neopterygii; Teleostei; Eutel
Acanthomorpha; Acanthopterygii; Percomorpha;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Q5B915;
                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406
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82661 MW;
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Emericella.
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Pred. No. 1e+
); Mismatches
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Euteleostei; Neoteleostei;
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    Hulme W., Irre.
A., Karatas A.,
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Best Local S
Matches 7
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Q4RWT8;
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13-SEP-2005 (TrEMBLrel. 31
13-SEP-2005 (TrEMBLrel. 31
13-SEP-2005 (TrEMBLrel. 31
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EMBL; CF
NON_TER
NON_TER
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                                                                                                                                             Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORFNames=GSTENG00027697001;
                                                                                                                              NUCLEOTIDE
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SEQUENCE 75
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EMBL; AACD01000049; E
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                             preliminary data.
L; CAAE01014981; CAG07144.1;
                                                                             CAUTION: The sequence
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                                                               EMBL/GenBank/DDBJ whole
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(FEB-2004) to the
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to the EMBL/GenBank/DDBJ
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Percomorpha; Tetraodontiformes;
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., Ozouf-Costaz C., Bernot J
utfalla G., Dossat C., Segui
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RESULT 9
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D6PCS4 BRARE PRELIMINARY;
ID Q6PCS4;
AC Q6PCS4;
DT 05-JUL-2004 (Tremblrel. 27,
DT 05-JUL-2004 (Tremblrel. 27,
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Aboukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
An Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
An Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
An Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
An Erickson J., Faro S., Graham L., Grand-Pierre N., Hafez N.,
An Agopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
An Agopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
An Arells C., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
An Kells C., Johnson R., Jones C., Kamal M., Kamat A., Karatas L.,
An Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
An Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
An Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
An Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
An Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
An Nielsen C.B., Schupback R., Seaman S., Severy P., Smirnov S.,
An Anchupka A., Ramassamy U., Raymond C., Retta R., Rise C., Rogov P.,
An Anahas J., Tesfaye S., Theodore J., Topham K., Travers M.,
An Alamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
An Alamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
An Anahas J., Tesfaye S., Theodore J., Topham K., Travers M.,
An Alamas J., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
An Anahas J., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein.
ORFNames=AN2724.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                        EMBL; AACD01000048; EAA63022.1;
Hypothetical protein.
SEQUENCE 1171 AA; 127986 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=FGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q5B9Q6_EMENI PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome Sequence of Aspergillus nidulans.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAUTION: The sequence shown here is derived EMBL/GenBank/DDBJ whole genome shotgun (WGS)
                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary data.
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Bastien V., Bloom T., Boguslavkiy
., Calvo S.E., Camarata J., Chang J
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Pred. No. 1.7e+02;
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                            sequence update)
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Q589W9 EMENI P
ID Q589W9;
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DT 10-MAY-2005 (T
DT 10-MAY-2005 (T
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                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
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; GO:0003677; ;
; GO:0005096; ;
; GO:0016491; ;
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                                 (TrEMBLrel.
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(TrEMBLrel.
                                                                                                                     PRELIMINARY;
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RX MEDLINE-2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RT Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.;
RT proc. Natl Acad Scii U.S. A 9016899-16901(2002)
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Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii;
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ORFNames=zgc:63950;
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Pfam; PF00620; RhoGAP; 1.
SMART; SM00109; C1; 1.
SMART; SM00324; RhoGAP; 1.
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                                                                                                                                                                                                                                                             PROSITE; PS00479; DAG PE_BIND_DOM_1; PROSITE; PS50081; DAG_PE_BIND_DOM_2; PROSITE; PS50238; RHOGAP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000198; InterPro; IPR012294;
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BC059184; AAH59184.1; -; mRNA.
ZDB-GENE-031010-44; ZGC:63950.
1 RRLPRTP 7
                                                                                                     Similarity
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1337 AA;
                                                                   Conservative
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F:DNA binding; IEA.
F:GTPase activator activity; IEA.
F:oxidoreductase activity; IEA.
P:intracellular signaling cascade; IEA.
                                                                                                 100.0%;
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RhoGAP
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; Craniata; Vertebrata; Eu
Teleostei; Ostariophysi;
                                                                Score 38; DB 2; Length 1337; Pred. No. 2e+02; ; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99:16899-16903(2002).
                                                                                                                                                                                                2061AE2507489079 CRC64;
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Ostariophysi; Cypriniformes;
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DT 10-MAY-2
DE Hypochet
GN ORFNames
OS Aspergill
OC Eukaryot
OC Eukaryot
OC Eukaryot
OC NCBI Tax
RN [1]
RP NUCLEOTI
RP STRAIN=F
RA Birren B
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RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook P., Corum B., DeArellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Gardyna S., Generre S., Graham L., Grand-Pierre N., Hafez N.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Kells C., Landers T., Levine R., Lindblad Toh K., Liu G., Lui A.,
RA Kells C., Landers T., Levine R., Lindblad Toh K., Liu G., Lui A.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicoll R.,
RA Mielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., Smirnov S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Nandam G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Nandam G., Zainoun J., Zembek L., Zimmer A., Zody M.,
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Matches 7
Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S., Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L., Boukhgalter B., Butler J., Calvo S.B., Camarata J., Chang J., Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R., Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N., Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
                                                                                                                                                                                                                                                Aspergillus nidulans FGSC A4.
Eukaryota; Fungi; Ascomycota;
Eurotiales; Trichocomaceae; E
                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
STRAIN=FGSC A4;
                                                                                                                                                                                                                          NCBI_TaxID=227321;
                                                                                                                                                                                                                                                                                                                Hypothetical protein. ORFNames=AN8648.2;
                                                                                                                                                                                                                                                                                                                                                         Q5AST2;
10-MAY-2005 (TrEMBLrel.
10-MAY-2005 (TrEMBLrel.
10-MAY-2005 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Q5AST2_EMENI PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome Sequence of Aspergillus nidulans.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=FGSC A4;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RRLPRTP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1538 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               693
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                a; Pezizomycotina; Eurotiomycetes; Emericella.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.4e+02;
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Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,

Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,

Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,

Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,

Milsen C., B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,

Nielsen C., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,

Nielsen C., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,

Nielsen C., Narbu C., O'Connor T., O'Donnell P., O'Neil D.,

Nielsen C., Narbu C., Phunkhang P., Pierre N., Purcell S.,

Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,

Rachupka A., Ramasamy U., Raymond C., Retta R., Severy P., Smirnov S.,

Raman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,

Maryman J., Schauer S., Theodore J., Topham K., Travers M.,

Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,

Vandar, Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,

Lander S., Schupback R., Sembek L., Zimmer A., Zody M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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 Pfam;
Pfam;
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Hypothetical
SEQUENCE 15
                                                                                                                8888
                                                                                                                                                                          EMBL; AF021263; AAB96629.1; HSSP; P14687; 1AMU.
                                                                                                                                                                                                                  MCHenney M.A., DeHoff B. Submitted (AUG-1997) to -!- SIMILARITY: Belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Daptomycin biosynthetic protein subunit (Fragment)
Streptomyces filamentosus (Streptomyces roseosporus
Bacteria; Actinobacteria; Actinobacteridae; Actinom
               InterPro; IPR010071; AA_adenyl_dom.
InterPro; IPR009081; ACP_like.
InterPro; IPR0009081; AMP-bind.
InterPro; IPR0001242; Condensatn.
InterPro; IPR006163; Phispanteth_bind.
InterPro; IPR006163; Phispantne S.
Pfam; PF00501; AMP-binding; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998
01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome Sequence of Aspergillus nidulans.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ
-!- CAUTION: The sequence shown here is derive
                                                                                                                                                                                                                                                              STRAIN=A21978.6;
                                                                                                                                                                                                                                                                               NUCLEOTIDE
                                                                                                                                                                                                                                                                                                          "Molecular cloning and physical mapping from Streptomyces roseosporus.";
J. Bacteriol. 180:143-151(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98083067; PubMed=9422604;
Mchenney M.A., Hosted T.J., Dehoff B.
                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=A21978.6;
                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=67294;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
STRFL
                                                                                                                GO:0048037; F:cofactor binding; IEA.
GO:0016874; F:ligase activity; IEA.
CO:0031177; F:phosphopantetheine bin
GO:0008152; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAUTION: The sequence sh
EMBL/GenBank/DDBJ whole
                                                                                                                                                                                                       family
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L; AACD01000158; E
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                                                                                                                                                                                                                                                                               SEQUENCE.
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1581 AA;
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   AMP-binding;
Condensation;
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Pred. No. 2.4e+02;
                                                                                                                                                                                      Genomic_DNA
                                                                                                                                                                                                                     ATP-dependent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence update)
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is derived from an
                                                                                                                               binding;
                                                                                                                                                                                                                                                                                                                                       of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                        roseosporus).
dae; Actinomycetales;
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                                                                                                                                                                                                                   AMP-binding
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                                                                                                                                 ΙEΑ
                                                                                                                                                                                                                                                                                                                                     daptomycin gene
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PF00550;

PP-binding;

PROO:

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Best Local
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                                            Query Match
Best Local
                                  Matches
                                                                                             InterPro; IPR001242; Condensatn.
InterPro; IPR001060; NRPS synth.
InterPro; IPR001060; NRPS synth.
InterPro; IPR001663; Pheptoyanteth_bd.
InterPro; IPR006162; Ppantne S.
InterPro; IPR006162; Ppantne S.
Pfam; PP00501; AMP-binding; 5.
Pfam; PP00505; PP-binding; 5.
Pfam; PP005050; PP-binding; 5.
Pfam; PR00154; AMPBINDING.
TIGRPAMs; TIGR0173; AA-adenyl-dom; 5.
PROSITE; PS000124; AMPBINDING; 5.
PROSITE; PS00075; AMPBINDING; 5.
PROSITE; PS00075; AMPBINDING; 5.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 5.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 5.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 5.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 5.
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PRINTS; PH
TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                        analysis of the gene cluster and
stereochemistry.";
Microbiology 151:1507-1523(2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50075; ACP_DOMAIN; 1.
PROSITE; PS00455; AMP_BINDING; 2.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomycineae;
NCBI_TaxID=67294;
                                                                                                                                                                                                                                                                                InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                             "Daptomycin biosynthesis in Streptomyces roseosporus: analysis of the gene cluster and revision of peptide
                                                                                                                                                                                                                                                                                                                                                                                    Baltz R.H.;
                                                                                                                                                                                                                                                                                                                                                                                               Martin
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=NRRL 11379;
Miao V., Coeffet-LeGal M.-F.,
                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces filamentosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide synthetase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q50E74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphopantetheine.
                                                                                                                                                                                                                                                                                                       EMBL; AY787762; AAX31557.1; -;
                                                                                                                                                                                                                                                                     InterPro; IPR010071; AA_adenyl_dom.
InterPro; IPR009081; ACP_like.
InterPro; IPR000873; AMP-bind.
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STRFL
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                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs
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                                                                                                                                                                                                                                                                                                                                                                                             S., Ford R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRFL
                                Similarity 7; Conserv
RRLPRTP 7
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TIGR01733; AA-adenyl-dom;
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1590
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                                 100.0%;
larity 100.0%;
Conservative (
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Actinobacteridae; Actinomycetales;
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                                 Score 38; DB
Pred. No. 1e+
0; Mismatches
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Pred. No. 2.4e+0;
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                                                                               B53232641B6EA34C CRC64;
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                                                                                                  UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                             M., Silva C.
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                                            1e+03;
                                                         ВВ
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                                                      2; Length 5830;
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"Generation and initial analysis of more than 15,000 full-length human T. and mouse CDNA securaces ""
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Q8WTX9; O15461;
28-FEB-2003 (Re
28-FEB-2003 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Zinc finger DHHC domain containing protein 1 (
[OHHC-domain-containing cysteine-rich protein
Name=ZDHHC1; Synonyms=Cl6orf1, ZNF377;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                        Putilina 7. Wong P., Gentleman S.;
Putilina T., Wong P., Gentleman S.;
"The DHHC domain: a new highly conserved cysteine-rich motif.";
Mol. Cell. Biochem. 195:219-226(1999).

-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

-i- TISSUB SPECIFICITY: Expressed at high levels in fetal lung, kidney
and heart. Expressed at lower levels in adult pancreas and lung.

-i- SIMILARITY: Contains 1 DHHC-type zinc finger.
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                                                                                                                                                                                                                                                                                                                    This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22388257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Pfam; PF01529; zf-DHHC; Ī.
ProDom; PD003041; Znf DHHC; 1.
PROSITE; P850216; ZF_DHHC; 1.
Metal-binding; Transmembrane; Zinc; Zinc-finger.
TRANSMEM 53 73 Potential.
                                                                                               HGNC; HGNC:17916; ZDHHC1.
GC; GC:0003677; F:DNA binding; NAS.
GC; GC:0005515; F:protein binding;
InterPro; IPR001594; Znf_DHHC.
                                                                                                                                                                                                EMBL; U90653; AAB86591.2;
HSSP; P28814; 1BW4.
                                                                                                                                                                                                                                       EMBL; BC021908; AAH21908.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99321009; PubMed=10395086; DOI=10.1023/A:1006932522197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse cDNA sequences.";
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                                                                                                                                                                               ENSG00000159714; Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                     -; mRNA.
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RESULT
PPN1_CF
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ZN FING
                                                                                                                                       EMBL; AE017345; AAW43547.1; -; Ge: InterPro; IPR004843; M-pesterase. Pfam; PF00149; Metallophos; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Cryptococcus neoformans."; Science 307:1321-1324(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cryptococcus neoformans (Filobasidiella neoformans).

Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;

Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPN1_CRYNE STANDARD; PRT; 678 AA. Q5KH67; Created) 10-MAY-2005 (Rel. 47, Created) 10-MAY-2005 (Rel. 47, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation update) Endopolyphosphatase (EC 3.6.1.10). Name=PPN1; OrderedLocusNames=CNE01080;
                                                                            Complete proteome; Glycoprotein; Hydrolase; Signal-anchor; Transmembrane; Vacuole.
TOPO DOM 1 2 Cytoplasmic (Potential).
TRANSMEM 3 23 Signal-anchor for type II mem
                                                                                                                                                                                                     removed.
                                                                                                                                                                                                                                                                                                                +
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                                                                                                                                                                                                                                                                                                 oligophosphate.
SUBCELLULAR LOCATION: Type II membrane protein. Vaculoar.
SUBCELLULAR LOCATION: Type II membrane protein. Vaculoar.
                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Catalyzes the hydrolysis of inorganic polyphosphate (poly P) chains of many hundreds of phosphate residues into shorter lengths (By similarity).

CATALYTIC ACTIVITY: Polyphosphate + n H(2)O = (n+1)
                                                                                                                                                                                                                                                                                            PTM: Processing by proteases in activation (By similarity).
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Cytoplasmic (Potential).
Signal-anchor for type II
protein (Potential).
Vacuolar (Potential).
N-linked (GlcNAC. . .) (P
N-linked (GlcNAC. . .) (P
N-linked (GlcNAC. . .) (P
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Pred. No. 1.6e+02;
1; Mismatches 0
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DHHC-type.
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N-linked (GlcNAc. . .) (Potential).
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OLOTON WHY THE REPORT SHAPE